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On nucleic - nucleic search, using sw model  
Run on: January 12, 2005, 05:06:55 ; Search time 2053 Seconds  
822.840 Million cell updates/sec

Title: US-10-001-254-5  
Perfect score: 294  
Sequence: 1 acatatgtgcgtgcctcaa.....tgctccagatgtttccc 294  
Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext: 1.0

Searched: 4300275 seqs, 2872944193 residues  
Total number of hits satisfying chosen parameters: 8600550  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
1: /cggn2\_6/pctodata/1/pubpna/us07\_pubcomb.seq:\*

2: /cggn2\_6/pctodata/1/pubpna/us06\_pubcomb.seq:\*

3: /cggn2\_6/pctodata/1/pubpna/us06\_pubtomb.seq:\*

4: /cggn2\_6/pctodata/1/pubpna/us06\_pubtomb.seq:\*

5: /cggn2\_6/pctodata/1/pubpna/us07\_new\_pub.seq:\*

6: /cen2\_6/pctodata/1/pubpna/pctus\_pubcomb.seq:\*

7: /cggn2\_6/pctodata/1/pubpna/us08\_new\_pub.seq:\*

8: /cen2\_6/pctodata/1/pubpna/us08\_pubcomb.seq:\*

9: /cggn2\_6/pctodata/1/pubpna/us09\_pubcomb.seq:\*

10: /cggn2\_6/pctodata/1/pubpna/us09\_pubtomb.seq:\*

11: /cggn2\_6/pctodata/1/pubpna/us09c\_pubtomb.seq:\*

12: /cggn2\_6/pctodata/1/pubpna/us09\_new\_pub.seq:\*

13: /cggn2\_6/pctodata/1/pubpna/us10\_pubtomb.seq:\*

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16: /cggn2\_6/pctodata/1/pubpna/us10c\_pubtomb.seq:\*

17: /cggn2\_6/pctodata/1/pubpna/us10c\_pubtomb.seq:\*

18: /cggn2\_6/pctodata/1/pubpna/us10\_new\_pub.seq:\*

19: /cggn2\_6/pctodata/1/pubpna/us11\_new\_pub.seq:\*

20: /cggn2\_6/pctodata/1/pubpna/usgo\_new\_pub.seq:\*

21: /cggn2\_6/pctodata/1/pubpna/usgo\_pubtomb.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	294	100.0	294	14 US-10-001-254-5 Sequence 5, Appl
2	294	100.0	1383	14 US-10-001-254-15 Sequence 15, Appl
3	294	100.0	2817	10 US-03-966-451-3 Sequence 3, Appl
4	294	100.0	2817	14 US-10-001-254-27 Sequence 27, Appl
5	294	100.0	2817	16 US-10-630-399-3 Sequence 3, Appl
6	292.4	99.5	1383	9 US-03-795-595-2 Sequence 2, Appl
7	292.4	99.5	1383	10 US-03-795-595-2 Sequence 2, Appl
8	241.6	82.2	501	9 US-09-833-790-149 Sequence 149, Appl
9	204.4	69.5	1542	9 US-09-795-595-4 Sequence 4, Appl
10	204.4	69.5	1542	10 US-09-795-595-4 Sequence 4, Appl
11	151.8	51.6	31000	10 US-03-966-451-10 Sequence 10, Appl
12	151.8	51.6	31000	16 US-10-630-399-10 Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-10-001-254-5  
; Sequence 5, Application US/10001254  
; Publication No. US2003004702A1  
GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loredana  
; APPLICANT: Lee, Sug Hyung  
; APPLICANT: Roth, Wilfred  
; APPLICANT: Steinmer-Liewen, Frank  
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins  
FILE REFERENCE: P-LJ 5037  
CURRENT APPLICATION NUMBER: US/10/001,254  
PRIOR APPLICATION NUMBER: 60/301,889  
CURRENT FILING DATE: 2001-11-15  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/715,893  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastS6Q for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 294  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(294)  
US-10-001-254-5

Query Match Similarity 100.0%; Score 294; DB 14; Length 294;  
Best Local Similarity 100.0%; Pred. No. 5,4e-75; Mismatches 0; Indels 0; Gaps 0;

**RESULT 2**  
US-10-001-254-15  
; Sequence 15, Application US/10001254  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loredana  
; APPLICANT: Lee, Sug Hyung  
; APPLICANT: Roth, Wilfred  
; TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins  
; FILE REFERENCE: P-LJ 5037  
; CURRENT APPLICATION NUMBER: US/10/001,254  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/301,889  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 15  
; LENGTH: 1383  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE: CDS  
; NAME/KEY: CDS  
; LOCATION: (50)...(1432)  
; US-10-001-254-15

Query Match 100.0%; Score 294; DB 14; length 1383;  
Best Local Similarity 100.0%; Pred. No. 1.1e-74; length 1383;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCCCTCAATGTTGACTAATTAGGAGCTCAGTTATGACCT 60  
Db 61 CAGAAGGAGGAAGAGTGTAGCTGTTACCTTAATAAACCATCTGGATGATAC 120  
QY 121 AATCAGTTCACATAGGAGATTGAAAGCATACTTCACACTGGAAAGTCCACTCT 180  
Db 121 AATCAGTTCACATAGGAGATTGAAAGCATACTTCACACTGGAAAGTCCACTCT 180  
QY 181 GAATACTGTTGACTGGGCACCAATGGAAAGTCCACTCT 240  
Db 181 GAATACTGTTGACTGGGCACCAATGGAAAGTCCACTCT 240  
QY 241 ATCCAAATGATGATTTCCTGGAGCTTGTCCC 294  
Db 241 ATCCAAATGATGATTTCCTGGAGCTTGTCCC 294

**RESULT 3**  
US-09-966-451-3  
; Sequence 3, Application US/09966451  
; Publication No. US20030087856A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION  
; FILE REFERENCE: RS-0324  
; CURRENT APPLICATION NUMBER: US/09/966,451  
; CURRENT FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 3  
; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: CDS  
; NAME/KEY: CDS  
; LOCATION: (50)...(1432)  
; US-09-966-451-3

Query Match 100.0%; Score 294; DB 10; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 1.5e-74; length 2817;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCCCTCAATGTTGACTAATTAGGAGCTCAGTTATGACCT 60  
Db 74 ACATATGCGCTGCCCTCAATGTTGACTAATTAGGAGCTCAGTTATGACCT 133  
QY 61 CAGAAGGAGGAAGAGTGTAGCTGTTACCTTAATAAACCATCTGGATGATAC 120  
Db 134 CAGAAGGAGGAAGAGTGTAGCTGTTACCTTAATAAACCATCTGGATGATAC 193  
QY 121 AATCAGTTCACATAGGAGATTGAAAGCATACTTCACACTGGAAAGTCCACTCT 180  
Db 194 AATCAGTTCACATAGGAGATTGAAAGCATACTTCACACTGGAAAGTCCACTCT 253  
QY 181 GAATACTGTTGACTGGGCACCAATGGAAAGTCCACTCT 240  
Db 254 GAATACTGTTGACTGGGCACCAATGGAAAGTCCACTCT 313  
QY 241 ATCCAAATGATGATTTCCTGGAGCTTGTCCC 294  
Db 314 ATCCAAATGATGATTTCCTGGAGCTTGTCCC 367

**RESULT 4**  
US-10-001-254-27  
; Sequence 27, Application US/10001254  
; Publication No. US20030049702A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loredana  
; APPLICANT: Lee, Sug Hyung  
; APPLICANT: Roth, Wilfred  
; TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins  
; FILE REFERENCE: P-LJ 5037  
; CURRENT APPLICATION NUMBER: US/10/001,254  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/301,889  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 27  
; SEQ ID NO 27

Query Match 100.0%; Score 294; DB 14; length 1383;  
Best Local Similarity 100.0%; Pred. No. 1.1e-74; length 1383;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCCCTCAATGTTGACTAATTAGGAGCTCAGTTATGACCT 60  
Db 25 ACATATGCGCTGCCCTCAATGTTGACTAATTAGGAGCTCAGTTATGACCT 84  
QY 61 CAGAAGGAGGAAGAGTGTAGCTGTTACCTTAATAAACCATCTGGATGATAC 120  
Db 85 CAGAAGGAGGAAGAGTGTAGCTGTTACCTTAATAAACCATCTGGATGATAC 144  
QY 121 AATCAGTTCACATAGGAGATTGAAAGCATACTTCACACTGGAAAGTCCACTCT 180  
Db 145 AATCAGTTCACATAGGAGATTGAAAGCATACTTCACACTGGAAAGTCCACTCT 204  
QY 181 GAATACTGTTGACTGGGCACCAATGGAAAGTCCACTCT 240  
Db 205 GAATACTGTTGACTGGGCACCAATGGAAAGTCCACTCT 264  
QY 241 ATCCAAATGATGATTTCCTGGAGCTTGTCCC 294

; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50)...(1429)  
; US-10-001-254-27

Query Match 100.0%; Score 294; DB 14; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 1.5e-74;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; Qy 1 ACATATGTCGCTGCCTCAATGTCGACTTAATTAGGAACCTGTCAAGTTTATGATCT 60  
; Db 74 ACATATGTCGCTGCCTCAATGTCGACTTAATTAGGAACCTGTCAAGTTTATGATCT 133  
; Qy 61 CAAGAAGGATGGAAGAAGTAGCTGATCTAGTAAACACCATCTGGATGATGATAC 120  
; Db 134 CAAGAAGGATGGAAGAAGTAGCTGATCTAGTAAACACCATCTGGATGATGATAC 193  
; Qy 121 ATACAGTTTCACATAGGAGATGAGCTACTCAAACTGAAAAGTCCACTCT 180  
; Db 194 ATACAGTTTCACATAGGAGATGAGCTACTCAAACTGAAAAGTCCACTCT 253  
; Qy 181 GAATTAATGTTGCTCGGACCAATGCCAACAGTGATCTTGATCTTG 240  
; Db 254 GAATTAATGTTGCTCGGACCAATGCCAACAGTGATCTTGATCTTG 313  
; Qy 241 ATCCAAATGATTTCCTCGAGCTTCTCCAGATGCGTTCCC 294  
; Db 314 ATCCAAATGATTTCCTCGAGCTTCTCCAGATGCGTTCCC 367

RESULT 5

US-10-630-399-3

Sequence 3, Application US/10630399

Publication No. US2004019009A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTI-SENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS

FILE REFERENCE: RTS-0324

CURRENT APPLICATION NUMBER: US/10/630,399

CURRENT FILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: US/09/966,451

PRIOR FILING DATE: 2001-09-28

NUMBER OF SEQ ID NOS: 88

SEQ ID NO 3

LENGTH: 2817

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (50)...(1432)

US-10-630-399-3

Query Match 100.0%; Score 294; DB 16; Length 2817;

Best Local Similarity 100.0%; Pred. No. 1.5e-74;

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 ACATATGTCGCTGCCTCAATGTCGACTTAATTAGGAACCTGTCAAGTTTATGATCT 60

; Db 74 ACATATGTCGCTGCCTCAATGTCGACTTAATTAGGAACCTGTCAAGTTTATGATCT 133

; Qy 61 CAAGAAGGATGGAAGAAGTAGCTGATCTAGTAAACACCATCTGGATGATGATAC 120

; Db 134 CAAGAAGGATGGAAGAAGTAGCTGATCTAGTAAACACCATCTGGATGATGATAC 193

; Qy 121 ATACAGTTTCACATAGGAGATGAGCTACTCAAACTGAAAAGTCCACTCT 180

; Db 194 ATACAGTTTCACATAGGAGATGAGCTACTCAAACTGAAAAGTCCACTCT 253

; Qy 181 GAATTAATGTTGCTCGGACCAATGCCAACAGTGATCTTGATCTTG 240

; CURRENT APPLICATION NUMBER: US/09/759,595

; CURRENT FILING DATE: 2001-01-13

; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50)...(1429)  
; US-09-795-595-2

Query Match 99.5%; Score 292.4; DB 9; Length 1383;  
Best Local Similarity 99.7%; Pred. No. 3.2e-74; Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; Qy 1 ACATATGTCGCTGCCTCAATGTCGACTTAATTAGGAACCTGTCAAGTTTATGATCT 60  
; Db 25 ACATATGTCGCTGCCTCAATGTCGACTTAATTAGGAACCTGTCAAGTTTATGATCT 84  
; Qy 61 CAAGAAGGATGGAAGAAGTAGCTGATCTAGTAAACACCATCTGGATGATGATAC 120  
; Db 85 CAAGAAGGATGGAAGAAGTAGCTGATCTAGTAAACACCATCTGGATGATGATAC 144  
; Qy 121 ATACAGTTTCACATAGGAGATGAGCTACTCAAACTGAAAAGTCCACTCT 180  
; Db 145 ATACAGTTTCACATAGGAGATGAGCTACTCAAACTGAAAAGTCCACTCT 204  
; Qy 181 GAATTAATGTTGCTCGGACCAATGCCAACAGTGATCTTGATCTTG 240  
; Db 205 GAATTAATGTTGCTCGGACCAATGCCAACAGTGATCTTGATCTTG 264  
; Qy 241 ATCCAAATGATTTCCTCGCGACTCTTGCTCCAGATGCTGTCTCC 294  
; Db 265 ATCCAAATGATTTCCTCGCGACTCTTGCTCCAGATGCTGTCTCC 318

RESULT 7

US-09-795-595-2

Sequence 2, Application US/0979595

Publication No. US2003005916A1

GENERAL INFORMATION:

APPLICANT: Wesche, Holger

APPLICANT: Li, Shiyun

APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use

FILE REFERENCE: 016781-003916US

CURRENT APPLICATION NUMBER: US/09/759,595

CURRENT FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395  
 PRIORITY FILING DATE: 2000-01-13  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 2  
 LENGTH: 1383  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)  
 LOCATION: (1)..(1383)  
 OTHER INFORMATION: human IRAK-4  
 US-09-759-595-2

Query Match Best Local Similarity 99.5%; Score 292.4; DB 10; Length 1383; Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ACATATGCGCTGCCTCAATGGACTAATTAGGAACSTGTAGATTTATGATCT 60
Db 25 ACTATGCGCTGCCTCAATGGACTAATTAGGAACSTGTAGATTTATGATCT 84
Db 61 CAAGBAGGTGAGAAGTGTAGCTTAATAAACCTCTGGATGATGATAC 120
Db 85 CAAGAGGTGAAAGTAGCTGTAGCTTAAAAACATCTGGATGATGATAC 144
Db 121 ATCAGTTTCACATAGGAGATTAGGATTAAGCATTTCAACTGGAAAAGTCCACTCT 180
Db 145 AACAGTTTCACATAGGAGATTAGGATTAAGCATTTCAACTGGAAAAGTCCACTCT 204
Db 181 GAACTACTGTTGACTGGGACACAAATGCAAGTGCAAGTGCTGATCTGGATCTTG 240
Db 205 GATTACTGTTGACTGGGACACCAATGCAAGTGCAAGTGCTGATCTGGATCTTG 264
Db 241 ATCCAAATGAATTTCCTCTCGCGAGCTTGTCCAGATGCTGTTCC 294
Db 265 ATCCAAATGAATTTCCTCTCGCGAGCTTGTCCAGATGCTGTTCC 318
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RESULT 8  
 US-09-833-790-149  
 Sequence 149, Application US/09833790  
 Patent No. US20020068288A1  
 GENERAL INFORMATION:  
 APPLICANT: Lodes, Michael J.  
 APPLICANT: Wang, Tongtong  
 APPLICANT: Sechrist, Heather  
 APPLICANT: Mohamath, Raodoh  
 APPLICANT: Indrias, Carol Y.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 FILE REFERENCE: 210121\_512  
 CURRENT APPLICATION NUMBER: US/09/833,790  
 CURRENT FILING DATE: 2001-04-11  
 NUMBER OF SEQ ID NOS: 440  
 SOFTWARE: FastSEQ for Windows Version 4.0.  
 SEQ ID NO: 149  
 LENGTH: 501  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(501)  
 OTHER INFORMATION: n = A,T,C or G

Query Match Best Local Similarity 81.0%; Score 204.4; DB 9; Length 1542; Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 1 ACATATGCGCTGCCTCAATGGACTAATTAGGAACSTGTAGATTTATGATCT 60
Db 187 ACATACATACGCAACCTTAATGGGATCTCTAGGAGCTGTGGATTTATGATCT 245
Db 61 CAAGAGGTGAGAAGTGTAGCTGTAGCTTAATAAACCTCTGGATGATGATAC 120
Db 247 CAGAGGTGAGAAGTGTAGCTGTAGCTTAATAAACCTCTGGATGATGATAC 306
Db 121 AACAGTTTCACATAGGAGATTAGGATTAAGCATTTCAACTGGAAAAGTCCACTCT 180
Db 307 ATCAGTTTCACATAGGAGATTAGGATTAAGCATTTCAACTGGAAAAGTCCACTCT 366
Db 181 GAACTACTGTTGACTGGGCCACAAATGCAAGTGCAAGTGCTGATCTGGATCTTG 240
Db 367 GAATCTGCTGTTGACTGGGCCACAACTGCAAGTGCTGATCTGGATCTTG 60
Db 241 ATCCAAATGAATTTCCTCTCGCGAGCTTGTCCAGATGCTGTTCC 294
Db 427 GTCCAGATGAGCTGTGCTCTGGGACACTTGCAAGTGCTGATCTGGATCTTG 480
```

RESULT 9  
 US-09-795-595-4  
 Sequence 4 Application US/09795595  
 Publication No. US20020039423A1  
 GENERAL INFORMATION:  
 APPLICANT: Wesche, Holger  
 APPLICANT: Li, Shyun  
 APPLICANT: Tularik Inc.  
 TITLE OF INVENTION: TRAK-4: Compositions and Methods of Use  
 FILE REFERENCE: 018781-003910US  
 CURRENT APPLICATION NUMBER: US/09/795,595  
 CURRENT FILING DATE: 2001-01-11  
 PRIOR APPLICATION NUMBER: US 60/176,395  
 PRIOR FILING DATE: 2000-01-13  
 NUMBER OF SEQ ID NOS: 7  
 SEQ ID NO: 4  
 LENGTH: 1542  
 TYPE: DNA  
 ORGANISM: Mus sp.

FEATURE:  
 OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)

Query Match Best Local Similarity 81.0%; Score 204.4; DB 9; Length 1542; Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 1 ACATATGCGCTGCCTCAATGGACTAATTAGGAACSTGTAGATTTATGATCT 60
Db 187 ACATACATACGCAACCTTAATGGGATCTCTAGGAGCTGTGGATTTATGATCT 245
Db 61 CAAGAGGTGAGAAGTGTAGCTGTAGCTTAATAAACCTCTGGATGATGATAC 120
Db 247 CAGAGGTGAGAAGTGTAGCTGTAGCTTAATAAACCTCTGGATGATGATAC 306
Db 121 AACAGTTTCACATAGGAGATTAGGATTAAGCATTTCAACTGGAAAAGTCCACTCT 180
Db 307 ATCAGTTTCACATAGGAGATTAGGATTAAGCATTTCAACTGGAAAAGTCCACTCT 366
Db 181 GAACTACTGTTGACTGGGCCACAAATGCAAGTGCAAGTGCTGATCTGGATCTTG 240
Db 367 GAATCTGCTGTTGACTGGGCCACAACTGCAAGTGCTGATCTGGATCTTG 60
Db 241 ATCCAAATGAATTTCCTCTCGCGAGCTTGTCCAGATGCTGTTCC 294
Db 427 GTCCAGATGAGCTGTGCTCTGGGACACTTGCAAGTGCTGATCTGGATCTTG 480
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## RESULT 10

US-09-759-595-4  
Sequence 4, Application US/09759595  
Publication No. US20030059916A1

GENERAL INFORMATION:  
APPLICANT: Wesche, Holger  
APPLICANT: Li, Shyun

APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use

CURRENT APPLICATION NUMBER: US/09/003910US  
CURRENT FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395  
PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1

SEQ\_ID NO 4  
LENGTH: 1542

ORGANISM: Mus sp.

FEATURE: OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)

FEATURE: OTHER INFORMATION: cDNA

FEATURE: LOCATION: (163)..(1542)

OTHER INFORMATION: murine IRAK-4

Query Match 69.5%; Score 204.4; DB 10; Length 1542;  
Best Local Similarity 81.0%; Pred. No. 1..le-48;  
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 1 ACATATGTCGGCTCGCTCAATGTTGACTATTAGGAAGCTGTGCGATTATTGATCC 60  
Db 187 ACATACATACGCAACTTATGTTGGGATCCTAGGAAGCTGTGCGATTATTGATCC 60

Qy 61 CAAGBAGGATGGAAGCTAGTCAGTTAAACCATGGGATGATAGATAC 120  
Db 247 CAAGAGGGTGGAAGAAATTAGCAGTAGCTATCAAAGCGTCCGGCACGAGATAC 120

Qy 121 ATCAGTTGCATAGGAGATTCAGATTACTTCAACTGAAAAGTCCACTCT 180  
Db 307 ATCAGTTGCATATAGGAGATTCAGCTTACCTCAGCGGAGAGCCACCTCT 180

Qy 181 GAATTACTGTTGACTGGGCCACCAAAATGACAGTGTGATCTTGGGATCTTG 240  
Db 367 GAATGCTGTTGACTGGGCCACCAAGCTGACAGTGTGACGACTTGTGATCTTG 240

Qy 241 ATCCAAATGATTTTGCTCTGGATCTTGTGTCAGATGCTTCCC 294  
Db 427 GTCCAGATGCTGCTTGCCTCCACTCTCCAGTGCGGAGATGCCPTTCCC 480

RESULT 11

US-09-666-451-10  
Sequence 10, Application US/09666451

Publication No. US20030087856A1  
GENERAL INFORMATION:

APPLICANT: C. Frank Bennett  
APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS FILE REFERENCE: RIS 0324  
CURRENT APPLICATION NUMBER: US/09/966,451  
CURRENT FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 88  
SEQ ID NO 10

LENGTH: 31000  
TYPE: DNA

FEATURE: TYPE: DNA

## RESULT 12

US-10-630-399-10  
Sequence 10, Application US/10630399  
Publication No. US20040019009A1

GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS

CURRENT APPLICATION NUMBER: US/10/630,399  
CURRENT FILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: US/09/966,451  
PRIOR FILING DATE: 2001-09-28

NUMBER OF SEQ ID NOS: 88  
SEQ ID NO 10  
LENGTH: 31000

TYPE: DNA  
FEATURE: TYPE: DNA

ORGANISM: Homo sapiens  
SEQ\_ID NO 10

Query Match 51.6%; Score 151.8; DB 16; Length 31000;  
Best Local Similarity 95.7%; Pred. No. 7..9e-33;  
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 123 TCAGTTGCATAGGAGATTCAGCTTACTTCAACTGAAAAGTCCACTCT 182  
Db 12953 TTACTTACTTAAAGGAAATTGAGCATACTTCAACTGAAAAGTCCACTCTGA 13012

Qy 183 ATTRACTGTTGACTGGGCCACCAAAATGACAGTGTGATCTTGGGATCTTG 242  
Db 13013 ATTACTGTTGACTGGGCCACCAAAATGACAGTGTGATCTTGGGATCTTG 13072

Qy 243 CCAAAATGATTTTGCTCTGGAGCTTGTCTCCAGAT 285  
Db 13073 CCATAATGATTTTGCTCTGGAGCTTGTCTCCAGAT 13115

## RESULT 13

US-10-001-254-25  
Sequence 25, Application US/10001254  
Publication No. US20030049702A1

GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Florentino, Lorena  
APPLICANT: Lee, Sung Hyung  
APPLICANT: Roth, Wilfred  
APPLICANT: Steiner-Liewen, Frank  
TITLE OF INVENTION: No. US20030049702A1 el Death Domain Proteins  
FILE REFERENCE: P-LJ 5037

CURRENT APPLICATION NUMBER: US/10/001,254  
CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/301,889

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/715,893

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25 LENGTH: 211.

TYPE: DNA

ORGANISM: Homo sapien

FEATURE: CDS

LOCATION: (1)...(177)

US-10-001-254-25

Query Match 46.8%; Score 137.6; DB 14; Length 211;

Best Local Similarity 97.2%; Pred. No. 1e-29; Mismatches 0; Indels 4; Gaps 0;

Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 60

Db 25 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 84

QY 61 CAAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 120

Db 85 CAAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 144

QY 121 AATCAGTTCCACATAAGGAGATT 144

Db 145 AATCAGTTCCACATAAGTGGT 168

RESULT 14 US-10-244-535A-26096

Sequence 26096, Application US/10242535A

Publication No. US2004013663A1

GENERAL INFORMATION: Sequence 26096, Application US/10242535A

APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: Patentin version 3.2

SEQ ID NO 26096 LENGTH: 470

TYPE: DNA

ORGANISM: Human

US-10-085-783A-26096

Query Match 46.8%; Score 137.6; DB 16; Length 470;

Best Local Similarity 97.2%; Pred. No. 1.5e-29; Mismatches 0; Indels 4; Gaps 0;

Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 60

Db 139 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 198

QY 61 CAAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 120

Db 139 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 258

Db 259 AATCAGTTCACATAAGGAGTT 282

RESULT 15 US-10-085-783A-26096

Sequence 26096, Application US/0085783A

Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: Patentin version 3.2

SEQ ID NO 26096 LENGTH: 470

TYPE: DNA

ORGANISM: Human

US-10-085-783A-26096

Query Match 46.8%; Score 137.6; DB 16; Length 470;

Best Local Similarity 97.2%; Pred. No. 1.5e-29; Mismatches 0; Indels 4; Gaps 0;

Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 60

Db 139 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 198

QY 61 CAAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 120

Db 139 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 258

QY 121 AATCAGTTCACATAAGGAGATT 144

Db 259 AATCAGTTCACATAAGTGGT 282

Search completed: January 12, 2005, 07:07:01  
Job time : 2055 secs

Query Match 46.8%; Score 137.6; DB 16; Length 470;

Best Local Similarity 97.2%; Pred. No. 1.5e-29; Mismatches 0; Indels 4; Gaps 0;

Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 60

Db 139 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 198

QY 61 CAAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 120

Db 139 ACAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 258

QY 121 AATCAGTTCACATAAGGAGATT 144

Db 139 ACAGAGGAGATGGAGAGTGTAGCTGTAGCTATTAAACCATCTGGATGATAGATAC 258

Query Match 46.8%; Score 137.6; DB 16; Length 470;

Best Local Similarity 97.2%; Pred. No. 1.5e-29; Mismatches 0; Indels 4; Gaps 0;

Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 60

Db 139 ACATATGTCGCGCTGCCCTCAATGTGGACTATTAGGAGCTGCAATTATGATCT 198

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Om nucleic - nucleic search, using sw model

Run on: January 12, 2005, 04:23:14 ; Search time 75 Seconds

Perfect score: US-10-001-254-5

Sequence: 1 acatatggcgccgcctcaa. .... tgttcccaagatgttac 294

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

Issued Patents NA:\*

1: /cgn2\_6/pctdata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/pctdata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/pctdata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/pctdata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/pctdata/1/ina/PCTUS\_Comb.seq: \*  
6: /cgn2\_6/pctdata/1/ina/backfile1.seq: \*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	294	100.0	833	US-09-166-350-10
2	294	100.0	833	US-09-166-350-10
3	151.8	51.6	31000	US-09-966-451-10
4	40.4	13.7	1879	US-09-601-091-1
5	40.4	13.7	1879	US-09-601-091-3
6	40.4	13.7	2024	US-09-398-395A-51
7	40.4	13.7	2024	US-09-887-586A-51
8	40.4	13.7	2024	US-09-895-752-51
9	40.4	13.7	2024	US-09-903-01B-51
10	40.4	13.7	2024	US-09-900-791-51
11	38.2	13.0	267	US-09-543-681A-1549
12	33.8	11.5	580073	US-08-535-528D-1
13	33.6	11.4	711	US-09-583-110-1653
14	33.6	11.4	2393	US-09-951-527-90
15	33.2	11.3	654	US-09-248-798A-236
16	33	11.2	64081	US-09-790-988-1
17	32.8	11.2	477	US-09-513-999C-32039
18	32.8	11.2	202001	US-09-734-674-3
19	32.6	11.1	1728	US-09-036-731A-1
20	32.6	11.1	2971	US-09-710-279-3449
21	32.4	11.0	1737	US-09-248-798A-2516
22	32.4	11.0	9844	US-09-791-211-10
23	32.2	11.0	4402	US-09-494-970A-135
24	32	10.9	2274	US-09-107-532A-3535
25	32	10.9	3012	US-09-976-594-422
26	32	10.9	3012	US-09-919-039-167
27	32	10.9	9834	US-08-956-17E-37

ALIGNMENTS

RESULT 1  
US-09-166-350-10  
Sequence 10, Application US/09166350A

GENERAL INFORMATION:  
Patient No. 6440663

APPLICANT: Scanlan, Matthew  
APPLICANT: Chen, Yao  
APPLICANT: Stockert, Elisabeth  
APPLICANT: Old, Lloyd  
APPLICANT: Jeger, Elke  
APPLICANT: Knuth, Alex

TITLE OF INVENTION: Renal Cancer Associated Antigens and  
FILE REFERENCE: L0461/051

CURRENT APPLICATION NUMBER: US/09/166,350A  
CURRENT FILING DATE: 1998-10-05  
EARLIER APPLICATION NUMBER: US 09/166,350  
EARLIER FILING DATE: 1998-10-05  
NUMBER OF SEQ ID NOS: 35

SOFTWARE: FabesEQ for Windows Version 3.0

SEQ ID NO 10  
SEQ LENGTH: 833  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-166-350-10

Query Match 100.0%; Score 294; DB 4; Length 833;  
Best Local Similarity 100.0%; Pred. No. 1. 1e-82; 0; Mismatches 0; Indels 0; Gaps 0;

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGGCGCTGCCTCAATGTTGGACTTAATTAGGAAGCTGTCAGATTGTGACCT 60

Db 74 ACATATGGCGCTGCCTCAATGTTGGACTTAATTAGGAAGCTGTCAGATTGTGACCT 133

QY 61 CAGAACAGATGAGAAAGTGTAGTGAGCTATAAAACCCCTGGATGATGATAGATAC 120

Db 134 CAGAACAGATGAGAAAGTGTAGTGAGCTATAAAACCCCTGGATGATGATAGATAC 193

QY 121 ATTCAGTTCACTAAGGAGTTGAAGCATRACTGCAACTCGAAAGTCCACTCT 180

Db 194 ATTCAGTTCACTAAGGAGTTGAAGCATRACTGCAACTCGAAAGTCCACTCT 253

QY 181 GAAATTACTGTTACTGGGCCACACAATGCACTGTTGGATCTGTGATCTTG 240

Db 254 GAATTACTGTTACTGGGCCACACAATGCACTGTTGGATCTGTGATCTTG 313

QY 241 ATCCAAATGAATTGCTCTGGAGTCCTTGCTCCAGATGTCGTGTC 294

Db 314 ATCCAAATGAATTGCTCTGGAGTCCTTGCTCCAGATGTCGTGTC 367

RESULT 2  
US-09-966-451-3

; Sequence 3, Application US/09966451

; Patent No. 6692959

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS

; CURRENT APPLICATION NUMBER: US/09/966, 451

; CURRENT FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 88

; SEQ ID NO 3

; LENGTH: 2817

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: CDS

; LOCATION: (50) .. (1432)

; US-09-966-451-3

Query Match 100.0%; Score 294; DB 4; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 1.9e-82; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGTTGGCTGCCTCAATGTGAGCTTATTAGGAGGTGTCGATTTATGATCT 60

Db 74 ACATATGTTGGCTGCCTCAATGTGAGCTTATTAGGAGGTGTCGATTTATGATCT 133

Qy 61 CAAGAGGAGTGAAGAAGTAGCTGACTTAAACATCGTGTGATGATAC 120

Db 134 CAAGAGGAGTGAAGAAGTAGCTGACTTAAACATCGTGTGATGATAC 193

Qy 121 ATCATGGTTACATAGGAGATTGAGCACTTCACAATGGAAGAAGTCCACTCT 180

Db 194 AATCAGTTTCACTAGGAGATTGAGCACTTCACAATGGAAGAAGTCCACTCT 253

Qy 181 GAATTACTGTTGACTGGGCCACCAAAATGACAGTGGTGAATCTGGATCTTG 240

Db 254 GAACTACTGTTGACTGGGCCACCAAAATGACAGTGGTGAATCTGGATCTTG 313

Qy 241 ATCCAAATGAAATTGCTCTCGACTTTCAGATGCTGCTTCC 294

Db 314 ATCCAAATGAAATTGCTCTCGACTTTCAGATGCTGCTTCC 367

RESULT 3  
US-09-966-451-10

; Sequence 10, Application US/09966451

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS

; FILE REFERENCE: RITS-0324

; CURRENT APPLICATION NUMBER: US/09/966, 451

; CURRENT FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 88

; SEQ ID NO 10

; LENGTH: 31000

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: CDS  
US-09-966-451-10

Query Match 51.6%; Score 151.8; DB 4; Length 31000;  
Best Local Similarity 95.7%; Pred. No. 2.3e-37; Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 123 TCGATTCACATAGGAGATTGAGCAACTTCAACTGAAAGTCCACTCTGA 182

Db 12953 TCTACTTCTTAAGGAGATTGAGCAACTTCAACTGAAAGTCCACTCTGA 13012

RESULT 4  
US-09-601-091-1

; Sequence 1, Application US/09601091

; Patent No. 6342380

; GENERAL INFORMATION:

; APPLICANT: Colby, S. M. et al.

; TITLE OF INVENTION: Germacrene C Synthase Gene of Lycopersicon Esculentum

; CURRENT APPLICATION NUMBER: US/09/601, 091

; PRIOR APPLICATION NUMBER: PCT/US99/02133

; CURRENT FILING DATE: 2000-09-19

; PRIOR FILING DATE: 1999-02-02

; PRIOR APPLICATION NUMBER: US 60/073, 579

; CURRENT APPLICATION NUMBER: US/09/601, 091

; PRIOR FILING DATE: 1999-02-02

; NUMBER OF SEQ ID NOS: 6

; SEQ ID NO 1

; LENGTH: 1879

; TYPE: DNA

; ORGANISM: Lycopersicon esculentum

; FEATURE: CDS

; LOCATION: (39) .. (1685)

; US-09-601-091-1

Query Match 13.7%; Score 40.4; DB 3; Length 1879;  
Best Local Similarity 50.5%; Pred. No. 0.0064; Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 45 AGATTTATGATCCCTCAAGAAGATGAGACTTCTGAGCTTAAANACCTC 104

Db 761 AGCTTCTAGTATCTACAGGAGTTGAGATTTGCAATAATATCATA 820

Qy 105 TGGTGTGATAGATACATGTCATAAGGAGATTGAGCATATTCTCAAATGG 164

Db 821 TCGAAGGACAGGTTGCTGAGCTTCTACTCTGATATAGGAGTTGTTGAGCCA 880

Qy 165 AAAAGTCCACTCTGAACTTGTGTTACTGGGCACACAAATGCAAGTTGTTGA 224

Db 881 ATATAGTCGCGACAAATGATGACAAAGTACTCHACCTAACCTCACATTAGAGA 940

Qy 225 TCTGTGAGCTT 238

Db 941 CACTTTGATGCTT 954

RESULT 5  
US-09-601-091-3

; Sequence 3, Application US/09601091

; Patent No. 6342380

; GENERAL INFORMATION:

; APPLICANT: Colby, S. M. et al.

; TITLE OF INVENTION: Germacrene C Synthase Gene of Lycopersicon Esculentum

; CURRENT APPLICATION NUMBER: US/09/601, 091

; CURRENT FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: PCT/US99/02133

; PRIOR FILING DATE: 1999-02-02

; PRIOR APPLICATION NUMBER: US 60/073, 579

; CURRENT APPLICATION NUMBER: US/09/601, 091

; PRIOR FILING DATE: 1999-02-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

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; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(1678)
; US-09-601-091-3

Query Match 13.7%; Score 40.4; DB 3; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066; Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 45 AGATTTATGATCCTCAAGAAGGATGGAAAGGTAGCTGAGTATAAACCATC 104
Db 754 AGAGCTTAGTGTCTACAGGTGGTGCAGAGTGGATTGCAATTAATCCATA 813
QY 105 TGGTGTAGTGTAGATAACAATCGTTCACATAGGATTCACATAGGATGGAACTACTCAAATCTGG 164
Db 814 TGCAAGAGAGACGGTGTGAGTGTACTCTGGATATTAGAGTGTATTGACCCAA 873
QY 165 AAAAGTCCCTCTCTGAATTACTGTTGACTGGGACCCAAATTGACACAGTGGTA 224
Db 874 ATATAGTCGCGAGAAATGATGACAAGTACTCAACTGACCTCCATTATGACCA 933
QY 225 TCTTGAGATCTT 238
Db 934 CACTTTGATGCTT 947

RESULT 6
US-09-398-395A-51
; Sequence 51, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398, 395A
; PRIOR APPLICATION NUMBER: 09/398, 395
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/130, 628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150, 262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 51
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(1675)
; OTHER INFORMATION: VFNT germacrene C synthase
; US-09-887-586A-51

Query Match 13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066; Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 45 AGATTTATGATCCTCAAGAAGGATGGAAAGGTAGCTGAGTATAAACCATC 104
Db 754 AGAGCTTAGTGTCTACAGGTGGTGCAGAGTGGATTGCAATTAATCCATA 813
QY 105 TGGTGTAGTGTAGATAACAATCGTTCACATAGGATTCACATAGGATGGAACTACTCAAATCTGG 164
Db 814 TGCAAGAGAGACGGTGTGAGTGTACTCTGGATATTAGAGTGTATTGACCCAA 873
QY 165 AAAAGTCCCTCTCTGAATTACTGTTGACTGGGACCCAAATTGACACAGTGGTA 224
Db 874 ATATAGTCGCGAGAAATGATGACAAGTACTCAACTGACCTCCATTATGACCA 933
QY 225 TCTTGAGATCTT 238
Db 934 CACTTTGATGCTT 947

RESULT 8
US-09-895-752-51
; Sequence 51, Application US/09895752
; Patent No. 655297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6552971, Joseph P.
; APPLICANT: Starks, Courtney M.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895, 752

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; PRIORITY APPLICATION NUMBER: 09/338, 395
; PRIORITY FILING DATE: 1999-05-17
; PRIORITY APPLICATION NUMBER: 60/100, 993
; PRIORITY FILING DATE: 1999-05-18
; PRIORITY APPLICATION NUMBER: 60/130, 628
; PRIORITY FILING DATE: 1999-04-22
; PRIORITY APPLICATION NUMBER: 60/150, 262
; PRIORITY FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 51
; LENGTH: 2024
; OTHER INFORMATION: VFNT germacrene C synthase
; US-09-895-752-51

Query Match          13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066; Mismatches 96; Indels 0; Gaps 0;
Matches 98; Conservative 0; MisMatches 96; Indels 0; Gaps 0;
Qy          45 AGATTATTATTCCTCAAGAGGAGTGAAGAAGTTAGCTTATTAACCATC 104
Db          754 AGACTTAGTGTCTTACAACGGTGGTGAAGATTTGCAATAATATCCATA 813
Qy          45 AGATTTTATGATCTCAAGAGGAGTGAAGAAGTTAGCTTATTAACCATC 104
Db          754 AGAGCTTAGTGTCTTACAACGGTGGTGAAGATTTGCAATAATATCCATA 813
Qy          105 TGGTGTATGATGATACATCGTTCACAGGAGATTAAGCTTAAACCATC 104
Db          814 TGCAAGAGACAGGTGGTGTACTCTGGTATTTGAGCTGTTTGACCAA 873
Qy          165 AAAAGTCCCACITCTGAATCTGTTGACTCTGAGATTTGCAATAATATCCATA 164
Db          814 TGCAAGAGACAGGTGGTGTACTCTGGTATTTGAGCTGTTTGACCAA 873
Qy          165 AAAAGTCCCACITCTGAATCTGTTGACTCTGAGATTTGCAATAATATCCATA 164
Db          874 ATATAGTCGGGAGAAAATGATGACAAAGTACTCAACCTGACCTCCATTGACGA 933
Qy          225 TCTTGTTGATCTT 238
Db          934 CACTTTGATGCTT 947
; RESULT 9
; US-09-903-012B-51
; Sequence 51, Application US/0903012B
; Patent No. 656956
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900, 797
; PRIORITY APPLICATION NUMBER: US/09/398, 395
; PRIORITY FILING DATE: 1999-09-17
; PRIORITY APPLICATION NUMBER: 60/130, 628
; PRIORITY FILING DATE: 1999-04-22
; PRIORITY APPLICATION NUMBER: 60/150, 262
; PRIORITY FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 51
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(1675)
; OTHER INFORMATION: VFNT germacrene C synthase
; US-09-900-797-51
; US-09-900-797-51
; Sequence 51, Application US/0900797
; Patent No. 656956
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900, 797
; PRIORITY APPLICATION NUMBER: US/09/398, 395
; PRIORITY FILING DATE: 1999-09-17
; PRIORITY APPLICATION NUMBER: 60/130, 628
; PRIORITY FILING DATE: 1999-04-22
; PRIORITY APPLICATION NUMBER: 60/150, 262
; PRIORITY FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 51
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(1675)
; OTHER INFORMATION: VFNT germacrene C synthase
; US-09-903-012B-51

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US-09-543-681A-1549  
; Sequence 1549, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709\_1\_002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 1549  
; LENGTH: 267  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
; US-09-543-681A-1549

Query Match 13.0%; Score 38.2; DB 4; Length 267;  
\* Best Local Similarity 61.6%; Pred. No. 0.013; Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 84 TGTAGCTTAAACCACTATGGTAGATGAGATACAATCAGTTACATAAGGAGATT 143  
Db 147 TGCAAGGTTAAATGACCTGCTGTGATTAAGTAAATTAACACCACTAGCT 206

QY 144 TGAACGATTACTTCAACTGAAAGTCCACTCTGA 182  
Db 207 AGATCGTTCTAAAGTGGAGCTACTTGTTGATGA 245

RESULT 12  
US-08-545-528D-1/c  
; Sequence 1, Application US/08545528D  
; Patent No. 6537773  
; GENERAL INFORMATION:  
; APPLICANT: Fraser et al.  
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment  
; Patent No. 6537773  
; TITLE OF INVENTION: Thereof, and Uses Thereof  
; FILE REFERENCE: PB193P1  
; CURRENT APPLICATION NUMBER: US/08/545,528D  
; CURRENT FILING DATE: 1995-10-19  
; PRIOR APPLICATION NUMBER: US 08/488,018  
; PRIOR FILING DATE: 1995-05-07  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 580073  
; TYPE: DNA  
; ORGANISM: Mycoplasma genitalium  
; US-08-545-528D-1

Query Match 11.4%; Score 33.6; DB 4; Length 711;  
\* Best Local Similarity 48.9%; Pred. No. 0.57; Matches 90; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 37 AACGTGTCAGATTATGATCCTCAAGAGGATGGAGAGTAGTGATGATTA 96  
Db 194 AACCTTTAGAACACAGAACAAAGACTCGCAACAAAAGGAGATTCATTAG 135

QY 97 AAACCATCTGGTGTGATGATACATGATCAGTTGCACATAGGAGATTGAGCATTT 156  
Db 134 ATAGGAACTATGATGATGCGCAATTACTGATGTTGAAATATGATATGATGATGATT 75

QY 157 CAACTGGAAAGTCCACTCTGAATTACTGTTGACTGGGCCACACAAATTGACA 216  
Db 74 GTTACTCTAAAGAAATATCTGCTRAATTGCAAAATAATTGAGACTAACACTTGACA 15

QY 217 GTTG 220  
Db 14 AATG 11

RESULT 14  
US-08-961-527-90/c  
; Sequence 90, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

Search completed: January 12, 2005, 05:40:47  
 Job time : 90 secs

NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36 373  
 REFERENCE/DOCKET NUMBER: PB340P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 90:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2393 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-961-527-90

Query Match 11.4%; Score 33.6; DB 4; Length 2393;  
 Best Local Similarity 48.9%; Pred. No 0.97; 0; Mismatches 94; Indels 0; Gaps 0;  
 Matches 90; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy	37	AAAGCTGTCAGATTATGGATCCCAAGAGGTGAGAAGACTGCTAGCTTAA	95
Db	1113	AACCTTTAGTAACCAACCGAACTAAAGACTCGCAACAAAGGAGATAATCCATTAG	1054
Qy	97	AAACCATCTGGTGAATGATAGATCAGTTAACAGAGGATTGAGATTACTT	156
Db	1053	ATAGGAACTAGTGATGTCATTACTGATTTGAAATATGTTATGTTAGCATGATT	994
Qy	157	CAAACTGGAAAAGTCCCACCTCTGAAATTACTGTGTTGACCTGGGCCACCMCAAATGCA	216
Db	993	GTTACTCTAAGAAATATCTGCTAAATTGCAATAATTGAGAGACTACACTGACA	934
Qy	217	GTGCG 220	
Db	933	AATG 930	

RESULT 15  
 US-08-248-796A-236  
 ; Sequence 236, Application US/09248796A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstock et al  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.132  
 CURRENT APPLICATION NUMBER: US/09/248,796A  
 CURRENT FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074,725  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096,409  
 PRIOR FILING DATE: 1998-08-13  
 NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 236  
 LENGTH: 654  
 TYPE: DNA  
 ORGANISM: Candida albicans  
 US-08-248-796A-236

Query Match 11.3%; Score 33.2; DB 4; Length 654;  
 Best Local Similarity 51.3%; Pred. No 0.74; 0; Mismatches 73; Indels 0; Gaps 0;  
 Matches 77; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy	85	GTAGCTTAAACCACTCTGGATGATAGATAACATGTTACATAAGGAGTT	144
Db	226	GTAGCAATCAGACACACGGAGACCGGTTAGTTGAACTGAAATGCCATTAAGAACAT	285
Qy	145	GAAGCTTACTTCAACTGGAAAAGTCCACTCTGTAATTACCTGTTGACTGGGCACC	204
Db	286	GCAGAAATTAAATGGAGATTGAGAAAGCCACTTGGATACCTAGTTAACAAANGCAGT	345
Qy	205	ACAAATGCCAACAGTTGGTGTGACTCTGTGGAT 234	
Db	346	AAGTAGTATGACTCCATGTTGTTACCAAGGAT	375

GenCore version 5.1.6  
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### Om nucleic - nucleic search, using sw model

Run on:

January 12, 2005, 03:33:48 ; Search time 1934 Seconds

5539.442 Million cell updates/sec

Title: US-10-001-254-5  
Perfect score: 294

Sequence: 1 acatatgtgcgtgcctcaa.....tgctccagatgtgttccc 294

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gbs1:\*

9: gb\_gbs2:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

\* Query Match Length DB ID Description

No. Score Match DB ID Description

1	294	100.0	859	4	BG164491	RESULT 1
2	292.4	99.5	811	4	BG164498	BG164491
3	273.2	92.9	821	7	CK459029	DEFINITION
4	267.2	90.9	719	2	BFF69681	602342061 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:45205 5', mRNA Sequence.
5	262.	89.1	402	2	BBE82619	ACCESSION
6	262.	89.1	665	7	CN788062	VERSION
7	261.	88.8	1383	9	A Y418791	KEYWORDS
8	258.4	87.9	1383	9	AY18792	EST.
9	220.	74.8	541	4	BGG91069	SOURCE
10	205.4	69.9	313	4	BW151935	ORGANISM
11	204.4	69.5	503	6	CA538859	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthorina; Primates; Catarrhini; Hominidae; Homo.
12	204.4	69.5	598	5	BQ552228	REFERENCE
13	204.4	69.5	610	2	BB663378	1 NIH_MCC http://mgc.nci.nih.gov/.
14	204.4	69.5	637	2	BB613447	2 NIH_MCC http://mgc.nci.nih.gov/.
15	204.4	69.5	638	6	BY721552	3 NIH_MCC http://mgc.nci.nih.gov/.
16	204.4	69.5	663	6	BY726858	4 NIH_MCC http://mgc.nci.nih.gov/.
17	204.4	69.5	676	2	BB613167	5 NIH_MCC http://mgc.nci.nih.gov/.
18	204.4	69.5	1161	3	AK020397	6 NIH_MCC http://mgc.nci.nih.gov/.
19	204.4	69.5	2481	3	AK020837	7 NIH_MCC http://mgc.nci.nih.gov/.
20	204.4	69.5	2810	3	AK02028	8 NIH_MCC http://mgc.nci.nih.gov/.
21	202.8	69.0	575	5	BX522921	9 NIH_MCC http://mgc.nci.nih.gov/.
22	198.8	67.6	265	2	AW436511	10 NIH_MCC http://mgc.nci.nih.gov/.
23	182.4	62.0	507	2	BB866698	11 NIH_MCC http://mgc.nci.nih.gov/.
24	182.2	62.0	1286	9	AY418793	12 NIH_MCC http://mgc.nci.nih.gov/.

### ALIGNMENTS

25	181.4	61.7	524	2	AWI06160	AWI06160 um23h11.Y
26	163.2	55.5	453	2	BB860349	BB860349
27	154.2	52.4	686	2	CN066297	CN066297 F20_Ag2_P
28	154.2	52.4	711	7	CN067840	CN067840 K20_Ag2_P
29	154.2	52.4	775	7	CN061000	CN061000 A22_Ag2_P
30	154.2	52.4	782	7	CN064552	CN064552 Ag2_P7_L2
31	147.6	50.2	852	5	BU20911	BU20911 603550834
32	144.4	49.1	600	1	AJ53616	AJ53616 AJ53616
33	144.4	49.1	670	1	AJ44781	AJ44781 AJ4781
34	141.8	48.2	417	7	COT8006	COT8006 BL008B_H0
35	139.8	47.6	540	1	AL69213	AL69213 DKC2P686K
36	139.6	47.5	505	2	BR82323	BR82323 160964_BA
37	139.4	47.4	606	1	AL647125	AL647125 AL47125
38	139.2	47.3	625	9	CE224557	CE224557 tigr-gsb-
39	137.9	46.8	284	1	AA114228	AA114228 znt5905_r
40	137.6	46.8	753	6	CD654941	CD654941 AGENCOURT
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42	134	45.6	2	BR238344	BR238344 60194613	
43	125.8	42.8	210	2	BE845841	BE845841 23716_BA
44	123.4	42.0	664	4	BU035962	BU035962 BU035962
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QY	1 ACATATGCGCTGCCCTCAATGTGGACTTAATTAGGAAGCTGTCGATTTATGATCT	60	Best Local Similarity 99.7%; Pred. No. 2.8e-70; Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	59 ACATATGCGCTGCCCTCAATGTGGACTTAATTAGGAAGCTGTCGATTTATGATCT	118	
QY	61 CAAGCAGGATGGAGAAGTAGTGTAGCTTAACTGTTGATGATGATC	120	
Db	119 CAAGCAGGATGGAGAAGTAGTGTAGCTTAACTGTTGATGATGATC	178	
QY	121 AATCAGTTTCACATAAGGAGATTAGCTTAACTGTTGATGATGATC	178	
Db	179 AATCAGTTTCACATAAGGAGATTAGCTTAACTGTTGATGATGATC	238	
QY	181 GAATTAATGAAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	240	
Db	239 GAATTAATGAAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	298	
QY	241 ATCCAAATGAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	294	
Db	299 ATCCAAATGAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	352	
RESULT 2			
LOCUS	BG616438	811	bases 1 to 811 mRNA sequence.
DEFINITION	BG616438	811 bp	mRNA linear EST 18-APR-2001
ACCESSION	60242772RI NIH_MGC_61	5,	Homo sapiens cdNA clone IMAGE:4773760
VERSION	1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 811) NIH-MGC http://mgc.ncbi.nih.gov/.		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph. D. Email: cgapsb-r@mail.nih.gov		
FEATURES			
source	Tissue Procurement: CLONETECH laboratories, Inc. cDNA Library Preparation: CLONETECH laboratories, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: ILMCM1645 row: P column: 17		
High quality sequence start: 3.			
High quality sequence stop: 613.			
Location/Qualifiers			
1. .811			
/organism="Homo sapiens"			
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/clone="IMGB:4773760"			
/tissue_type="embryonal carcinoma"			
/lab_host="D110B (T1 phage-resistant)"			
/clone_lib="NIH_MGC_61"			
/note="Organ: testis; Vector: pBNR-LIB (Clontech); site_1: SfI (ggccctatggcc); site_2: SfI (ggccctatggcc); site_1: Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCAGGGCCGAGGCCGACAG-3', and 3' adaptor sequence: 5'-ATTCAGGGCCGAGGCCGACAG-3'. Where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb), 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."			
Query Match			
ORIGIN	99.5%; Score 292.4; DR 4; Length 811.		
Db	233 ATCATATGCGCTGCCCTCAATGTGGACTTAATTAGGAAGCTGTCGATTTATGATCT	60	
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LOCUS	CK459029	821	bases 1 to 821 mRNA sequence.
DEFINITION	CK459029 MARC 4PIG Sus scrofa cdNA 5'		EST 14-JAN-2004
ACCESSION	CK459029		
VERSTON	CK459029.1		
KEYWORDS	EST.		
SOURCE	Sub scrofa (pig)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1 (bases 1 to 821)		
AUTHORS	Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.B. and Keele, J.W.		
TITLE	Title: Porcine EST collection using a normalized library constructed from embryos representing early developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Smith, TPL		
FEATURES			
source	USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov		
Single pass sequencing. Bases called with phred v0.020495.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0 990229.			
Seq primer: GATATGCACTACATAGGG.			
Location/Qualifiers			
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/organism="Sus scrofa"			
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/tissue_type="pooled"			
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/note="Vector: pCDNA3.1; site_1: EcoRI; Site 2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."			
Query Match			
ORIGIN	92.9%; Score 273.2; DB 7; Length 821.		
Db	281 Best Local Similarity 95.6%; Pred. No. 5.9e-65; Mismatches 0; Indels 0; Gaps 0; Matches 281; Conservative 0; Mi matches 13; Insert 0; Gaps 0;	60	
QY	1 ACATATGCGCTGCCCTCAATGTGGACTTAATTAGGAAGCTGTCGATTTATGATCT	60	
Db	77 ACATATGCGCTGCCCTCAATGTGGACTTAATTAGGAAGCTGTCGATTTATGATCT	136	
QY	61 CAAGCAGGATGGAGAAGTAGTGTAGCTTAACTGTTGATGATGATC	120	
Db	119 CAAGCAGGATGGAGAAGTAGTGTAGCTTAACTGTTGATGATGATC	178	
QY	121 AATCAGTTTCACATAAGGAGATTAGCTTAACTGTTGATGATGATC	178	
Db	179 AATCAGTTTCACATAAGGAGATTAGCTTAACTGTTGATGATGATC	238	
QY	181 GAATTAATGAAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	240	
Db	239 GAATTAATGAAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	298	
QY	241 ATCCAAATGAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	294	
Db	299 ATCCAAATGAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	352	
RESULT 4			
LOCUS	CK459029	821	bases 1 to 821 mRNA sequence.
DEFINITION	CK459029 MARC 4PIG Sus scrofa cdNA 5'		EST 14-JAN-2004
ACCESSION	CK459029		
VERSTON	CK459029.1		
KEYWORDS	EST.		
SOURCE	Sub scrofa (pig)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1 (bases 1 to 821)		
AUTHORS	Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.B. and Keele, J.W.		
TITLE	Title: Porcine EST collection using a normalized library constructed from embryos representing early developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Smith, TPL		
FEATURES			
source	USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov		
Single pass sequencing. Bases called with phred v0.020495.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0 990229.			
Seq primer: TWW8032. row: K column: 23			
Location/Qualifiers			
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Query Match			
ORIGIN	92.9%; Score 273.2; DB 7; Length 821.		
Db	281 Best Local Similarity 95.6%; Pred. No. 5.9e-65; Mismatches 0; Indels 0; Gaps 0; Matches 281; Conservative 0; Mi matches 13; Insert 0; Gaps 0;	60	
QY	1 ACATATGCGCTGCCCTCAATGTGGACTTAATTAGGAAGCTGTCGATTTATGATCT	60	
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QY	61 CAAGCAGGATGGAGAAGTAGTGTAGCTTAACTGTTGATGATC	120	
Db	119 CAAGCAGGATGGAGAAGTAGTGTAGCTTAACTGTTGATGATC	178	
QY	121 AATCAGTTTCACATAAGGAGATTAGCTTAACTGTTGATGATC	178	
Db	179 AATCAGTTTCACATAAGGAGATTAGCTTAACTGTTGATGATC	238	
QY	181 GAATTAATGAAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	240	
Db	239 GAATTAATGAAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	298	
QY	241 ATCCAAATGAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	294	
Db	299 ATCCAAATGAATTGCTCCGGAGCTTGCTCCAGATGCTGTTCC	352	
RESULT 5			
LOCUS	CK459029	821	bases 1 to 821 mRNA sequence.
DEFINITION	CK459029 MARC 4PIG Sus scrofa cdNA 5'		EST 14-JAN-2004
ACCESSION	CK459029		
VERSTON	CK459029.1		
KEYWORDS	EST.		
SOURCE	Sub scrofa (pig)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1 (bases 1 to 821)		
AUTHORS	Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.B. and Keele, J.W.		
TITLE	Title: Porcine EST collection using a normalized library constructed from embryos representing early developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Smith, TPL		
FEATURES			
source	USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov		
Single pass sequencing. Bases called with phred v0.020495.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0 990229.			
Seq primer: TWW8032. row: K column: 23			
Location/Qualifiers			
1. .821			
/organism="Sus scrofa"			
/mol_type="mRNA"			
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Query Match			
ORIGIN	92.9%; Score 273.2; DB 7; Length 821.		
Db	281 Best Local Similarity 95.6%; Pred. No. 5.9e-65; Mismatches 0; Indels 0; Gaps 0; Matches 281; Conservative 0; Mi matches 13; Insert 0; Gaps 0;	60	

Qy	61	CAGAAGAGATGGAGAAGTAGTGTAGCTTAAACATCTGTCGATGATAC	120
Db	152	CAGAAGAGATGGAGAAGTAGTGTAGCTTAAACATCTGTCGATGATAC	211
Db	121	AATCAGTTCACTATAAGGAGATTGAGCATTACTCACAATGAAAAGTCCATCTG	180
Db	353	AACCGTTTCATAGAGGATCTGAGGATTACTCAACTGGAAGATGCCACTGT	412
Qy	181	GAATTACTGTGACTGGGACCAATGCACAGTGATCTGTGATCTTG	240
Db	413	GAATTACTGTGACTGGGACCAATGCACAGTGATCTGTGATCTTG	472
Qy	241	ATCCAAATGAAATTTCCTGGGACTCTTGTCTCCAGATGCTGTCCC	294
Db	473	GTCCAATGAGTTTGGCCCTGCAAGTCCTTGCTCCAGATGCTGTCCC	526
RESULT 4	BF696981		
LOCUS	BF696981	719 bp mRNA linear EST 22-DEC-2000	
DEFINITION	602130160P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287014 5'		
mRNA sequence.			
REFERENCE	BP696981		
VERSION	BP696981.1	GI:11982389	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 719)		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact : Robert Strausberg, Ph.D.		
COMMENT	Email: cgabbs-r@mail.nih.gov		
CDNA Library Preparation:	ATCC		
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNL)		
DNA Sequencing by:	Incyre Genomics, Inc.		
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov		
Plate:	LICW1124 row: g column: 15		
High quality sequence stop:	632.		
location/Qualifiers			
FEATURES	source		
	1. .719		
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	/clone="IMGR:4287014"		
	/tissue_type="primitive neuroectoderm"		
	/lab_host="DHL0B (T1 phage-resistant)"		
	/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcgcc); Site_2: SfiI (ggccattttggcc);		
	Double-stranded cDNA was cloned from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGACCC-3', and 3' adaptor sequence: 5'-ATTTAGGCGGAGGGGCCACAG-dT(30)RN-3', where B = A, C, or G, and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). Average contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."		
ORIGIN			
Query Match	90.9%; Score 267.2; DB 2; Length 719;		
Best Local Similarity	98.3%; Pred. No. 2.7e-63;		
Matches	291; Conservative 0; Mismatches 3; Indels 2; Gaps 2;		
Qy	1	ACATATGCGCGCTCTGATGTTGAAATTAGGAGCTGTGAGATTATGCTCT	60
Db	92	ACATATGCGCGCTCTGATGTTGAAATTAGGAGCTGTGAGATTATGCTCT	151
RESULT 5	BE482619		
LOCUS	BE482619	402 bp mRNA linear EST 27-MAR-2003	
DEFINITION	16843 BARC 5B0V Bos taurus cDNA 5', mRNA sequence.		
REFERENCE	BP482619		
VERSION	BE482619.1	GI:9602152	
KEYWORDS	EST.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
REFERENCE	1 (bases 1 to 402)		
AUTHORS	Sonstegard, T., Capuccio, A.V., White, J., Van Tassel, C.P., Wells, K.D., Connor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Quackenbush, J.		
TITLE	Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index		
JOURNAL	Mamm. Genome 13 (7), 373-379 (2002)		
MEDLINE	2215956		
PUBLMED	1210684		
COMMENT	Contact: Sonstegard TS USDA, ARS, Beltsville Agricultural Research Center Bldg. 200 Rm 2A, Beltsville, MD 20705, USA Tel: 301 504 8416 Fax: 301 504 8414 Email: tads@psb1.barc.usda.gov		
PCR PRIMERS	Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.		
FORWARD	AGGAGACAGCTATGCGAT		
BACKWARD	GTTTCCCCAGTCAGACG		
Plate	11 row: F column: 7		
Seq primer	ATTAGGAGACCTATAG.		
FEATURES	source		
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	/organism="Bos taurus"		
	/mol_type="mRNA"		
	/db_xref="taxon:9913"		
	/tissue_type="pooled"		
	/lab_host="DHL0B"		
	/clone_id="BARC 5B0V"		
	/note="Vector: pcMV SP016; Site_1: NotI; Site_2: SalI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."		
ORIGIN			
Query Match	89.1%; Score 262; DB 2; Length 402;		
Best Local Similarity	93.2%; Pred. No. 6.7e-62;		
Matches	274; Conservative 0; Mismatches 20; Indels 0; Gaps 0;		
Qy	1	ACATATGCGCGCTCTGATGTTGAAATTAGGAGCTGTGAGATTATGCTCT	60

Db	88	ACATAGTGCGCTGCTCAGTCCTGCGACTTATTAGAAGCTGTCCGATTATTATCCT	147	Best Local Similarity 93.2%; Pred: No. 7.3e-62;
Qy	61	CAAGAGGATGGAAGAACGTTAGTCCTGCTTGCAGTAATTAGAAACCATCTCGTGATGATAC	120	Matches 274; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Db	148	CAAGAGGATGGAAGAACGTTAGTCCTGCTTGCAGTAATTAGAAACCATCTCGTGATGATAC	120	1 ACATAGTGCGCTGCTCAGTCCTGCGACTTATTAGAAGCTGTCCGATTATTATCCT 60
Qy	121	AATCGTTTCACATAGGAGATTAGCTTACCTCAACTGGAAAAGTCCCCTCT	180	ACATAGTGCGCTGCTCAGTCCTGCGACTTATTAGAAGCTGTCCGATTATTATCCT 128
Db	208	AATCGTTTCACATAGGAGATTAGCTTACCTCAACTGGAAAAGTCCCCTCT	180	61 CAAGAGGATGGAAGAACGTTAGTCCTGCTTGCAGTAATTAGAAACCATCTCGTGATGATAC 120
Qy	181	GATTACTGTTGACTGGGCCACCAATTGCAAGTGGATCTGGAATGTTG 240	129 CAAGAGGATGGAAGAACGTTAGTCCTGCTTGCAGTAATTAGAAACCATCTCGTGATGATAC 188	
Db	268	GAGTACTGTTGACTGGGCCACCAATTGCAAGTGGATCTGGAATGTTG 327	121 AATCGTTTCACATAGGAGATTAGCTTACCTCAACTGGAAAAGTCCCCTCT 180	
Qy	241	ATCCAAATGATTGTCCTGGGACCAATTGCAAGTGGATCTGGAATGTTG 294	189 AATCGTTTCACATAGGAGATTAGCTTACCTCAACTGGAAAAGTCCCCTCT 248	
Db	328	GTCCAAATGAGTTTGGCCCTGCAAGTCTTGTCTTACAGATGCTTACCC	381	181 GATTACTGTTGACTGGGCCACCAATTGCAAGTGGATCTGGAATGTTG 240
Qy	328	GTCCAAATGAGTTTGGCCCTGCAAGTCTTGTCTTACAGATGCTTACCC	381	249 GAGTACTGTTGACTGGGCCACCAATTGCAAGTGGATCTGGAATGTTG 308
Db	328	GTCCAAATGAGTTTGGCCCTGCAAGTCTTGTCTTACAGATGCTTACCC	381	241 ATCCAAATGATTGTCCTGGGACCAATTGCAAGTGGATCTGGAATGTTG 294
Qy	328	GTCCAAATGAGTTTGGCCCTGCAAGTCTTGTCTTACAGATGCTTACCC	381	309 GTCCAAATGAGTTTGGCCCTGCAAGTCTTGTCTTACAGATGCTTACCC 362
RESULT 6	CNT788062	CNT788062	CNT788062	DEFINITION mRNA linear EST 26-MAY-2004
LOCUS	CNT788062	CNT788062	CNT788062	VERSION CNT788062.1
DEFINITION	CNT788062	CNT788062	CNT788062	KEYWORD EST.
ACCESSION	CNT788062	CNT788062	CNT788062	SOURCE
VERSION	CNT788062.1	CNT788062	CNT788062	ORGANISM
KEYWORDS				TITLE
JOURNAL				Intestinal Muscle and Epithelial Tissues of Holstein Cattle
COMMENT				Author(s): Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumelli, L.K.
FEATURES	source	source	source	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
source				Publ: 162; BARC-EAST, Beltsville, MD 20705, USA
source				Tel: 3015048904
source				Fax: 3015048944
source				Email: rbaumann@anri.barc.uda.gov
source				Single pass sequencing. Bases called and trimmed with phred 0.00025 using options -tim_alt "-trim_fasta. Vector identified by cross match using options -minmatch 12 -minscore 18
source				Plate: 26 row: O column: 07 Seq primer: CCTATTTAGGAGCACTATAGAAC
source				High Quality sequence stop: 666.
source				Location/Qualifiers
source				1. .666
source				/organism="Bos taurus"
source				/mol_type="mRNA"
source				/strains="Holstein"
source				/db_xref="taxon:9913"
source				/clone=8BOV_260077
source				/sex="Female"
source				/tissue_type="Epithelial, Muscle"
source				/dev_stage="Lactating, Neonatal"
source				/lab_host="D110B_Tona"
source				/clone_lib="BARC 8BOV"
source				Note: Organ: Intestine; Vector: pcMVSPORT6.1; Site_1: Noti; Site_2: EcorI; Normalized cow cDNA intestinal library in pcMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestine, 1 neonatal intestine, 4/5 lactating proximal duodenum, Jejunum, distal ileum, Colon, 1/5 neonatal, proximal duodenum, Jejunum, distal ileum"
ORIGIN				COMMENT
				These sequences were made by sequencing genomic exons and ordering them based on alignment.
FEATURES	source	source	source	FEATURES
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source				1. .1383
source				/organism="Homo sapiens"
source				/mol_type="genomic DNA"
source				/db_xref="taxon:9606"
source				/gene="IRAK4"
source				/locus_tag="HOM6675"
ORIGIN				Query Match Best Local Similarity 88.8%; Score 261; DB 9; Length 1383; Matches 261; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy	1	1	1	1 ACATAGTGCGCTGCTCAATGTTGACTTATTAGAAGCTGTCCGATTATTATCCT 60

QY	61	CAAGAAGGAGTGAAGAGTTAGCTGTAGCTATAAACACATCTGGATGATGATAC	120	OY	181	GAATTACTGTTCACTSGGGACCAAAATCCACAGTTGGATCTTGATCTTG	240
Db	85	CAAGAAGGAGTGAAGAGTTAGCTGTAGCTATAAACACATCTGGATGATAC	144	Db	205	GAAATTACTGTTCACTGGGGACCAAAATCCACAGTTGGATCTTGATCTTG	264
OY	121	ATCAGTTTCACAATAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	180	OY	241	ATCCAAATGAATTGCTCGGGATCTTGATCTTGATCTTGATCTTG	294
Db	145	ATCAGTTTCACAATAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	204	Db	265	ATCCAAATGAATTGCTCGGGATCTTGATCTTGATCTTGATCTTG	318
OY	181	GAATTACTGTTGACTGGGCCACAAATTGACAGTGGATCTGATCTTG	240	RESULT 9	BG991069	BG991069	
Db	205	GAATTACTGTTGACTGGGCCACCAAAATTGACAGTGGATCTGATCTTG	264	LOCUS	340084	BARC 5B0V	Bos taurus cDNA 5', mRNA sequence.
OY	241	ATCCAAATGAATTGCTCGGGATCTTGATCTTGATCTTGATCTTG	294	DEFINITION	340084	BARC 5B0V	Bos taurus cDNA 5', mRNA sequence.
Db	265	ATCCAAATGAATTGCTCGGGATCTTGATCTTGATCTTGATCTTG	318	ACCESSION	BG691069.1	GI:13932889	
RESULT 8	AT418792	AY418792	1383 bp DNA linear GSS 17-DRC-2003	VERSION	BG691069.1	GI:13932889	
LOCUS	AT418792	Pan troglodytes	Pan troglodytes (chimpanzee)	KEYWORDS	Bos taurus (cow)	Bos taurus	
DEFINITION	AY418792	Pan troglodytes IRAKA gene, virtual transcript, partial sequence, genomic survey sequence.	SOURCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buttheria; Primates; Cattarrhini; Hominidae; Pan.	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buttheria; Primates; Cattarrhini; Hominidae; Pan.	
ACCESSION	AY418792	AY418792.1	GI:39774752	REFERENCE	1 (bases 1 to 541)	Mammalia; Bovidae;	
VERSION	AY418792.1	GI:39774752	AUTHORS	Clark,A.G., Gianoowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanebaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrara,S., Wang,G., Zheng,X.H., White,T.J., Spinks,J.J., Adams,M.D. and Cargill,M.	AUTHORS	Connor,B.E., Cho,J., Sultana,R., shade,L., Wray,J.B., Wells,K.D. and Quackenbush,J.	
REFERENCE	1	(bases 1 to 1383)	TITLE	Analyses of bovine mammary gland EST and functional annotation of the Bos taurus gene index	JOURNAL	Mamm. Genome 13 (7), 373-379 (2002)	
AUTHORS	1	(bases 1 to 1383)	COMMENT	12140684	COMMENT	12140684	
PUBLISHED	14671302	Clark,A.G., Gianoowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanebaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrara,S., Wang,G., Zheng,X.H., White,T.J., Spinks,J.J., Adams,M.D. and Cargill,M.	CONTACT	Sonstegard TS	JOURNAL	Science 302 (5652), 1960-1963 (2003)	
REFERENCE	2	(bases 1 to 1383)	USDA, ARS, Beltsville Agricultural Research Center	PUBMED	1213956	PUBMED	
AUTHORS	2	(bases 1 to 1383)	Bldg. 200 Rm 2A, Beltsville, MD 20705, USA	COMMENT	1213956	COMMENT	
JOURNAL	Submitted (16-Nov-2003)	Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	PHONE	301 504 8416	PHONE	301 504 8416	
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.	These sequences were made by sequencing genomic exons and ordering them based on alignment.	FAX	301 504 8414	FAX	301 504 8414	
FEATURES	source	Location/Qualifiers	EMAIL	tads@psi.barc.usda.gov	EMAIL	tads@psi.barc.usda.gov	
FEATURES	source	Location/Qualifiers	Single Pass Sequencing	Bases called and alt(trimmed with phred v0.90904 e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.	Single Pass Sequencing	Bases called and alt(trimmed with phred v0.90904 e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.	
JOURNAL	Submitted (16-Nov-2003)	Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	FORWARD	AGGAACAGCTATGACCAT	FORWARD	AGGAACAGCTATGACCAT	
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.	BACKWARD	GTTTCCCACTCACGAGC	BACKWARD	GTTTCCCACTCACGAGC	BACKWARD	GTTTCCCACTCACGAGC
FEATURES	source	Location/Qualifiers	PLATE	100	PLATE	100	PLATE
FEATURES	source	Location/Qualifiers	ROW	B	ROW	B	ROW
FEATURES	source	Location/Qualifiers	COLUMN	15	COLUMN	15	COLUMN
FEATURES	source	Location/Qualifiers	1..541		1..541	1..541	1..541
FEATURES	source	Location/Qualifiers	/organism=Bos taurus	/mol_type="mRNA"	/organism=Bos taurus	/mol_type="mRNA"	/organism=Bos taurus
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FEATURES	source	Location/Qualifiers	/tissue_type="pooled"	/tissue_type="pooled"	/tissue_type="pooled"	/tissue_type="pooled"	/tissue_type="pooled"
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FEATURES	source	Location/Qualifiers	/clone_lib="BARC 5B0V"	/clone_lib="BARC 5B0V"	/clone_lib="BARC 5B0V"	/clone_lib="BARC 5B0V"	/clone_lib="BARC 5B0V"
FEATURES	source	Location/Qualifiers	library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
ORIGIN			ORIGIN		ORIGIN		ORIGIN
FEATURES	source	Location/Qualifiers	Query Match	74.8%	Query Match	74.8%	Query Match
FEATURES	source	Location/Qualifiers	Best Local Similarity	93.9%	Best Local Similarity	93.9%	Best Local Similarity
FEATURES	source	Location/Qualifiers	Pred. No.	3.2e-50	Pred. No.	3.2e-50	Pred. No.
FEATURES	source	Location/Qualifiers	Mismatches	0;	Mismatches	0;	Mismatches
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FEATURES	source	Location/Qualifiers	Matches	229;	Matches	229;	Matches
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FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
FEATURES	source	Location/Qualifiers	87.9%;	Score	258.4;	Score	258.4;
FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
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FEATURES	source	Location/Qualifiers	No.	0;	Indels	0;	No.
FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Gaps	0;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Matches	15;	Gaps
FEATURES	source	Location/Qualifiers	States	0;	Indels	0;	States
FEATURES	source	Location/Qualifiers	Score	220;	Score	220;	Score
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FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
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FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Indels	0;	Gaps
FEATURES	source	Location/Qualifiers	States	0;	Gaps	0;	States
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FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
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FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
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FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Indels	0;	Gaps
FEATURES	source	Location/Qualifiers	States	0;	Gaps	0;	States
FEATURES	source	Location/Qualifiers	Score	220;	Score	220;	Score
FEATURES	source	Location/Qualifiers	DB	4;	DB	4;	DB
FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
FEATURES	source	Location/Qualifiers	74.8%;	Score	258.4;	Score	258.4;
FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
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FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Indels	0;	Gaps
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FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
FEATURES	source	Location/Qualifiers	74.8%;	Score	258.4;	Score	258.4;
FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
FEATURES	source	Location/Qualifiers	Pred.	0;	Mismatches	35;	Pred.
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FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
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FEATURES	source	Location/Qualifiers	States	0;	Gaps	0;	States
FEATURES	source	Location/Qualifiers	Score	220;	Score	220;	Score
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FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
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FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
FEATURES	source	Location/Qualifiers	Pred.	0;	Mismatches	35;	Pred.
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FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Indels	0;	Gaps
FEATURES	source	Location/Qualifiers	States	0;	Gaps	0;	States
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FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
FEATURES	source	Location/Qualifiers	74.8%;	Score	258.4;	Score	258.4;
FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
FEATURES	source	Location/Qualifiers	Pred.	0;	Mismatches	35;	Pred.
FEATURES	source	Location/Qualifiers	No.	0;	Indels	0;	No.
FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Indels	0;	Gaps
FEATURES	source	Location/Qualifiers	States	0;	Gaps	0;	States
FEATURES	source	Location/Qualifiers	Score	220;	Score	220;	Score
FEATURES	source	Location/Qualifiers	DB	4;	DB	4;	DB
FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
FEATURES	source	Location/Qualifiers	74.8%;	Score	258.4;	Score	258.4;
FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
FEATURES	source	Location/Qualifiers	Pred.	0;	Mismatches	35;	Pred.
FEATURES	source	Location/Qualifiers	No.	0;	Indels	0;	No.
FEATURES	source	Location/Qualifiers	Mismatches	0;	Gaps	0;	Mismatches
FEATURES	source	Location/Qualifiers	Indels	0;	Matches	15;	Indels
FEATURES	source	Location/Qualifiers	Gaps	0;	Indels	0;	Gaps
FEATURES	source	Location/Qualifiers	States	0;	Gaps	0;	States
FEATURES	source	Location/Qualifiers	Score	220;	Score	220;	Score
FEATURES	source	Location/Qualifiers	DB	4;	DB	4;	DB
FEATURES	source	Location/Qualifiers	Length	541;	Length	541;	Length
FEATURES	source	Location/Qualifiers	74.8%;	Score	258.4;	Score	258.4;
FEATURES	source	Location/Qualifiers	Best Local Similarity	88.1%;	Pred. No.	8.3e-61;	Best Local Similarity
FEATURES	source	Location/Qualifiers	Pred.	0;	Mismatches	35;	Pred.
FEATURES	source	Location/Qualifiers	No.	0;			

Db	121	CCCCACGTGAGTACTGTGACTGGGCACCAAAATGCCACAGTTGTCAGATTGATCT	180	Db	77	ACATATGCGCTGCCATGTTGGACTANTAGGAAGCTGTCAGATTATGATCCT	136
Qy	231	GGATCTTTGATCCAAATGATTGTTGCTGCAAGCTTCTCCAGATGCTGT	290	Qy	61	CAGAAAGATGAGAGTTAGCTGNGCTTAACCATCTGGATGATACTAC	120
Db	181	GGATATTGGTCCAAATGAGTTTGCCCTGCAAGCTTCTGAGATGCTGT	240	Db	137	CAGAAAGATGAGAGTTAGCTGNGCTTAACCATCTGGATGATACTAC	196
Qy	291	TCCC 294		Qy	121	ATCAGTTCACTAAGGAGTTGAGCACTACTCAACTGAAAGTCCACTCT	180
Db	241	ACCC 244		Db	197	AATCAGTTCACTAAGGAGTTGAGCACTACTCTACTGGAAGATCCACTCT	256
<b>RESULT 10</b>							
	BM151935	BM151935	313 bp mRNA linear EST 30-NOV-2001				
	DEFINITION		TCBAP11457 Pediatric pre-B cell acute lymphoblastic leukemia sequence.				
	VERSION		BM151935.1				
	KEYWORDS		Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP145, mRNA EST.				
	ORGANISM		Homo sapiens (human)				
	REFERENCE		I (bases 1 to 313)				
	AUTHORS		Wei, Y., Tsang, M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr., Margolin, J.F., Guanarathne, P.H., Muzyk, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.				
	TITLE		Pediatric Leukemia cDNA Sequencing Project (2001)				
	JOURNAL		Unpublished (2001)				
	COMMENT		Contact: Dr. Judith F. Margolin at Baylor Children's Cancer Center and Human Genome Sequencing Center 1102 Bates MC3-320 Houston, TX 77030, USA Tel: 822-824-4533 Fax: 832-825-4038 Email: clones@xccc.org Seq primer: M13 primer Location/Qualifiers 1. .313 /organism="Homo sapiens"				
	FEATURES		/source				
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	/dev_stage="pediatric 2 years"		/lab_host=DHLOB				
	/lab_id=BamHI		leukemia, Baylor-HGSC project=TCBA" /note="Vector: Lambda psB, Site_1: BamHI; Site_2: ECOLI; First strand cDNA was primed with an anchored XbaI-oligo(dt) primer [5'GGAGACCTGAGCCGGAGGGAGG(T)VN 3'; V=A,C,G; N=A,C,G] and then dG tailed. Second strand was primed with a BamHI-DC primer [5'-AGAGAGCTGGATCCGGCGCAATATAT(C) 3'].				
	and directionally cloned into the BamHI and Sall sites of lambda psB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carinelli, P., Westover, A., Nishi-Yama, Y., Ohsumi, T., Itoh, M., Nagao, S., Sasaki, O., Okazaki, Y., Muramatsu, M., Schneider, C., Hayashiaki, Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"		Double-stranded cDNA was then digested with BamHI and XbaI and directionally cloned into the BamHI and Sall sites of lambda psB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carinelli, P., Westover, A., Nishi-Yama, Y., Ohsumi, T., Itoh, M., Nagao, S., Sasaki, O., Okazaki, Y., Muramatsu, M., Schneider, C., Hayashiaki, Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"				
	ORIGIN		Query Match Best Local Similarity 92.7%; Pred. No. 3.3e-46; Matches 215; Conservative 0; Mismatches 17; Indels 0; Gaps 0;				
	Qy		1 ACATATGCGCTGCCTCAATGCTGACTTATTAGAACGTTGTCAGATTGATCCT	60			
	Ex Tag Polymerase (Takara) with a primer Sal4-S. The		7 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to LoneLinker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using				

products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sall and NotI enzymes and cloned into Sall/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

## ORIGIN

Query Match 69.5%; Score 204.4; DB 6; Length 503;  
Best Local Similarity 81.0%; Pred. No. 6.8e-46; Indels 0; Gaps 0;  
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 1 ACATATGCGCTGCCTCAAGTGTGACTTAATTAGAAGCTGTGAGATTATGATCT 60  
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Qy 61 CAAGAGGAGTGAAGAGTGTAGCTGAGCTTAAAAAACCATCTCGTGATGATGATC 120  
Db 252 CAAGAGGGGGAGAAGAATTGAGCTAGTCATAAAAGCCGTCGGGAGGACAGATAC 311

Qy 121 ATACAGTTCACTAGGAGATTGAGCAATCTCAAAACTGGAAACTCCACTCT 180  
Db 312 ATACAGTTCACTATAGGAGATTGAGCAATCTCAAAACTGGAAACTCCACTCT 371

Qy 181 GAATTAATGTTGACTGGGACACCAAAATGCAAGTGTGATCTTGATGATCTT 240  
Db 372 GAACTGTGTTGACTGGGACACCAAAATGCAAGTGTGATCTTGATGATCTG 431

Qy 241 ATCCAATGATTITGCCTCGAGCTTGTCTCCAGAGTGTCTTCC 294  
Db 432 GTCCAGATTGAGCTGTTGCCCGCCACTCTCCCTGCGGATGCCGTTCC 485

## RESULT 12

LOCUS B052228 598 bp mRNA linear EST 20-JUN-2002  
DEFINITION R4014C09-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cdna clone  
ACCESSION B052228  
VERSION B052228.1 GI:21453114  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 528)

REFERENCE 1 Martin,P.R., Stagg,C.A., Babsey,U., Alba,K., Hamatani,T., Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.

AUTHORS Karayannidis, V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse CDNA clone set  
JOURNAL Genome Res. 12 (12), 1999-2003 (2002)  
MEDLINE 22354164  
PUBLMED 12466305  
COMMENT Contact: Yong Qian

Query Match 69.5%; Score 204.4; DB 5; Length 598;  
Best Local Similarity 81.0%; Pred. No. 7.e-46; Indels 0; Gaps 0;  
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy 61 CAAGAGGAGTGAAGAGTGTAGCTGAGCTTAAAAAACCATCTCGTGATGATC 120  
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Db 296 ATACAGTTCACTATAGGAGATTGAGCTAGTCATAAAAGCCGTCGGGAGGACAGATAC 355

Qy 181 GAATTAATGTTGACTGGGACACCAAAATGCAAGTGTGATCTTGATGATCTT 240  
Db 356 GAACTGTGTTGACTGGGACACCAAAATGCAAGTGTGATCTTGATGATCTG 415

Qy 241 ATCCAATGATTITGCCTCGAGCTTGTCTCCAGAGTGTCTTCC 294  
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## RESULT 13

LOCUS BB660378 610 bp mRNA linear EST 26-OCT-2001  
DEFINITION BB660378 RIKEN full-length enriched, 13 days embryo lung Mus  
ACCESSION BB660378  
VERSION BB660378.1 GI:16494199  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 610)

REFERENCE 1 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramatsu,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tegawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Tope,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

TITLE Unpublished (2001)  
JOURNAL Contact: Yoshihide Hayashizaki

COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-ras@gsc.riken.jp/ Carninci,P., Shibusawa,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new gene. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.

## FEATURES

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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGGAGGATTCGAGTAAATTAACTCCCCCCCCC 3']. cDNA was cloned into the XbaI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

## ORIGIN

Query Match 69.5%; Score 204.4; DB 2; Length 637;  
Best Local Similarity 81.0%; Pred. No. 7.1e-46;  
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Db 193 AGCATACATGCCACCTTAATGGGATCCTTATGATCCT 252  
QY 61 CAAGAGGAGTAGGAGAAGTGTAGCTTAAACATCTGGATGATGATC 120  
Db 253 CAAGAGGGGTGGAGAAATTAGCAGTACTGATCACAMAGGGTCGGGAGACAGATC 312  
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Db 433 GTCCAGATTGAGCTGTTGCCCGCACTCTCTGCTGCCGATGCCGTTCCC 486

## RESULT 15

BY211552 LOCUS BY211552 RIKEN full-length enriched, adult male diencephalon Mus DEFINITION musculus cDNA clone 9330209D03 5', mRNA sequence.

VERSION BY721552.1 GI:27134669  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Bilateria; Radiata; Sciuromorphi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 638)  
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nakaido,I., Osato,N., Saito,R., Suzuki,H., Yamamoto,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Balzarelli,R., Hill,D.P., Built,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batyalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corrini,L.E., Cousins,S., Dalla,B., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Glas,C., Godzik,A., Gough,J., Grimmord,S., Gubinich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawakawa,Y., Kozdzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchlomni,L., McKenzie,J., Mikii,H., Nagashima,T., Numata,K., Okido,T., Pavon,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C.A., Setou,M., Shimada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tonita,M., Verardo,R., Wagner,L., Wahnestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynn-Boris,A., Yangisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimme,A., Carninci,P., Hayatsu,N., Hirokane-Kishikawa,K., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiroki,T., Wakai,K., Kawai,J., Akawa,K., Arakawa,T., Fukuda,S., Hiyama,K., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Iwahashi,W., Hayashida,K., Hirozane,T., Hori,F., Fukuda,S., Habilume,W., Hayashida,K., Hirozane,T., Kojima,Y., Inotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsoa,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watanuki,A., Muramatsu,M. and Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)  
RIKEN Integrated sequence analysis (RISSA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in Riken contributed to preparation of experimental animal research in Riken. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
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note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGGAGGAGGATTCGAGCTTGTGTTGTTGTTWVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGGAGGATTCGAGCTTGTGTTGTTGTTGTTWVN 3']. cDNA was cloned into the XbaI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"

## ORIGIN

```

Query Match          69.5%;  Score 204.4;  DB 6;  Length 638;
Best Local Similarity 81.0%;  Pred. No. 7.1e-46;
Matches 238;  Conservative 0;  Mismatches 56;  Indels 0;  Gaps 0;
Qy      1 ACATATGCGGTGCCCTCAATGTTGACTAATTAGGAGCTGAGATTATTTGATCT 60
Db      198 ACATACATACGCCAACCTTAATGTTGGGATCTTAGGAAGCTGTTGGATTTATGATCT 257
Qy      61 CAGAAGGATGGAAAGATTAGTGTAGCTTAAAAAACATCTGGTGTAGTAGATAC 120
Db      258 CAAGAAGGGTSGAGAATTAGCAGTGCTTCAGAAAGCCGTTCCGGGAGACAGATAC 317
Qy      121 ATCAGTTTCACTAAGGAGATTGAAAGCATTTCAACTTGAAAAAGTGCCACTTCT 180
Db      318 ATCAGITCCATAAGGAGATTCGAAGCCATTCTCAGACCGGAAGAGCCCACCTGT 377
Qy      181 GATTTAGTGTGACTGGGACCAAAATGCCACAGTGATCTGTTGATCTTTG 240
Db      378 GAACTGCTGTGACTGGGACCAAGCTGACAGTGACGTTGGAATCTACTG 437
Qy      241 ATCCAAATGATTITTGCTCTGGAGTCCTTGCTCCAGATGCTGTCC 294
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Job time : 1944 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on:

January 12, 2005, 03:27:57 ; Search time 316 Seconds

4883.955 Million cell updates/sec

Title: US-10-001-254-5

Perfect score: 294

Sequence: 1 acatatgtgcgtgcctcaa.....tgctccacatgtgtttcc 294

Scoring table: IDENTITY\_NUC

GapOp 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001s:\*

5: geneseqn2002s:\*

6: geneseqn2003s:\*

7: geneseqn2002bs:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2003csb:\*

11: geneseqn2003db:\*

12: geneseqn2003ds:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

ADD-0074

ID ADD-0074 Standard; cDNA; 294 BP.

XX

AC ADD-0074;

XX

DT 22-OCT-2002 (first entry)

XX

DE Human IRAK4 DD (death domain) cDNA.

XX

KW Human; death domain; DD: death effector domain; DED: Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ss.

XX

OS Homo sapiens.

XX

## Key FH

FT CDS

1. .294

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/note= "No start and stop codon"

/note= "Partial"

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/note= "Human IRAK4 DD"

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Aah37656 Peppermin Aah37656 Peppermin  
Add1264 Bacterial Add45156 Human gen  
Add21602 Human sof Add21602 Human sof  
Add13431 Human thy Add13431 Human thy  
Add72207 Rice gene Add72207 Rice gene  
Aah4804 Internal Aah4804 Internal  
Add39523 Prokaryot Add39523 Prokaryot  
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Add58840 Continuation (5 of Add58840 Continuation (5 of  
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PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX

PS

XX

CC

KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;  
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;  
KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.  
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CC PA (GODZIK A.  
CC PA (PAWLICKI K.  
CC PA (FIORI/) FIORENTINO L.  
CC PA (LEES/) LEE S H.  
CC PA (ROTH/) ROTH W.  
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XX PI Stenner-Liewen F,  
XX DR WPI; 2002-50022/53.  
XX P-PSDB; AAB38897.  
XX PT New polypeptide comprising a death domain or death effector domain,  
XX useful for discovery of drugs that suppress infection, inflammation,  
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
XX PS Claim 18; Page 33-34; 99pp; English.

CC The present invention provides novel death Domain (DD) and death effector domain (DEB) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDP) DD and neural growth factor receptor-interacting death domain (NIRD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DEB or NB-ARC domain from Dp3, IRAK4, CTDP, DEB4 or NIRD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DEB or NB-ARC domain with protein that binds the DD, DEB or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial domains and/or anti-DD, anti-DEB or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allograft rejection, sepsis and other diseases. DD, DEB or NB-ARC domain proteins are used to treat infection, allergy, hyperplasia, neoplasia, keloid, benign prostatic hyperplasia, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK-4 DD cDNA).

SQ Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 294;  
Best Local Similarity 100.0%; Pred. No. 1..4e-77;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 294;  
Best Local Similarity 100.0%; Pred. No. 1..4e-77;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCCCTCAATGTGGACTTAATTAGGAAGCTGICAGATTTATGACCT 60  
 DB 1 ACATATGTCGCCCTCAATGTGGACTTAATTAGGAAGCTGICAGATTTATGACCT 60  
 QY 61 CAAGAGAGATGGAAGAAGTGTAGCTTAGTAAACACCCTCTGGATGATAGATC 120  
 DB 61 CAAGAGAGATGGAAGAAGTGTAGCTTAGTAAACACCCTCTGGATGATAGATC 120  
 QY 121 ATCAGTTTCACTAGGAGATTTGAACTACTTCAACTGCAAAGTCCACTCT 180  
 DB 121 ATCAGTTTCACTAGGAGATTTGAACTACTTCAACTGCAAAGTCCACTCT 180  
 QY 181 GAATTAATGTTGACTGGGACCCACAAATGCAAGTGGATCTTGATCTTG 240  
 DB 181 GAATTAATGTTGACTGGGACCCACAAATGCAAGTGGATCTTGATCTTG 240  
 QY 241 ATCCAAATGATTTTGGCTCTGGAGCTTGTGCTCCAGATGCTGTTCCC 294  
 DB 241 ATCCAAATGATTTTGGCTCTGGAGCTTGTGCTCCAGATGCTGTTCCC 294  
 RESULT 3  
 AAA09319  
 AAA09319 standard; DNA; 833 BP.  
 XX  
 AC  
 XX  
 AC  
 DT 10-AUG-2000 (first entry)  
 DB Human cancer associated antigen precursor DNA, clone NY-REN-64.  
 XX  
 KW renal cancer; cancer associated antigen precursor; diagnosis; cytostatic;  
 KW SS.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 50..670 /\*tag= a  
 XX  
 WO200020587-A2.  
 PD 13-APR-2000.  
 XX  
 PP 04-OCT-1999; 99WO-US022873.  
 XX  
 PR 05-OCT-1998; 98US-00166300.  
 PR 05-OCT-1998; 98US-00166350.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Obata Y, Gout I, Tureci O, Sahin U, Pfreundschuh M, Scanlan MJ;  
 PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A;  
 XX  
 DR WPI; 2000-303774/26.  
 DR P-PSDB; AAY92347.  
 XX  
 PT Preventing, diagnosing and/or treating disorders associated with abnormal expression of human cancer associated antigens.  
 XX  
 PS Claim 57; Page 85; 121pp; English.  
 XX  
 CC AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10-4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated with abnormal expression of human cancer associated antigens. The method comprises contacting a sample from a subject with an agent that specifically binds to the nucleic acid molecule or expression product (or fragment) complexed with a human leukocyte antigen (HLA) molecule and determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder  
 XX

SQ Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 294; DB 3; Length 833;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-77;  
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCCCTCAATGTGGACTTAATTAGGAAGCTGICAGATTTATGACCT 60  
 DB 74 ACATATGTCGCCCTCAATGTGGACTTAATTAGGAAGCTGICAGATTTATGACCT 133  
 QY 61 CAAGAGAGATGGAAGAAGTGTAGCTTAGTAAACACCCTCTGGATGATAGATC 120  
 DB 134 CAAGAGAGATGGAAGAAGTGTAGCTTAGTAAACACCCTCTGGATGATAGATC 193  
 QY 121 ATCAGTTTCACTAGGAGATTTGAACTACTTCAACTGCAAAGTCCACTCT 180  
 DB 194 ATCAGTTTCACTAGGAGATTTGAACTACTTCAACTGCAAAGTCCACTCT 253  
 QY 181 GAATTAATGTTGACTGGGACCCACAAATGCAAGTGGATCTTGATCTTG 240  
 DB 254 GAATTAATGTTGACTGGGACCCACAAATGCAAGTGGATCTTGATCTTG 313  
 QY 241 ATCCAAATGATTTTGGCTCTGGAGCTTGTGCTCCAGATGCTGTTCCC 294  
 DB 314 ATCCAAATGATTTTGGCTCTGGAGCTTGTGCTCCAGATGCTGTTCCC 367

RESULT 4  
 ADA0079  
 ID ADA0079 standard; DNA; 1383 BP.  
 XX  
 AC  
 XX  
 DT 22-OCT-2002 (first entry)  
 XX  
 DE Human IRAK4 gene #1.  
 XX  
 KW Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 1..1383 /\*tag= a  
 XX  
 FT CDS /\*product= "Human IRAK4"  
 XX  
 PN WO200240680-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 15-NOV-2001; 2001WO-US044844.  
 XX  
 PR 17-NOV-2000; 2000US-00715893.  
 PR 29-JUN-2001; 2001US-0301889P.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
 PI Steiner-Liewen F;  
 XX  
 DR WPI; 2002-500222/53.  
 DR P-RDDB; AAB24859.  
 XX  
 PT New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
 XX  
 PS Claim 19; Page 180-182; 209pp; English.

The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a domain that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (chlamydia trachomatis NIDD (NGFR-interacting Death Domain), with a candidate binding agent detecting the association of the domain and the candidate binding agent by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specific reactivity with CTDD DD of *C. trachomatis*, *C. muridarum*, *C. pneumoniae*, and *C. Psittaci* or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 gene sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other; XX SQ

	Query Match	Best Local Similarity	Score	DB	Length
QY	100.0%	294;	DB 6;	Length 1383;	
Matches	294;	Conservative 0;	Pred. No. 2, 3e-77;	Mismatches 0;	Indels 0;
Db	1 ACATAGTGGCGTCCTGAGTGGACTAATTAGGAAAGCTGTCGATTATTCATCCT	6			
QY	25 ACATAGTGGCGTCCTGAGTGGACTAATTAGGAAAGCTGTCGATTATTCATCCT	8			
Db	61 CAAAGAGATGGAGAGTGTAGCTGTAGTTAAAAAACCATCTGGTAGATAC	1			
QY	85 CAAGAAGGATGGAGAGTGTAGCTGTAGTTAAAAAACCATCTGGTAGATAC	1			
QY	121 ATTCAGTTCACTAAGGAGATTGAACTACTCAACTGAAAGTCCCTCT	1			
Db	145 ATTCAGTTCACTAAGGAGATTGAACTACTCAACTGAAAGTCCCTCT	1			
QY	181 GAATTCTGTGTTGACTGGGACCAAAATGCACTGTGATCTTGATCTTG	2			
Db	205 GAATTCTGTGTTGACTGGGACCAAAATGCACTGTGATCTTGATCTTG	2			
QY	241 ATCCCAAATGATTTTGCTCTGGAGCTTTGCTCCAGATGCTGTTCCC	294			
Db	265 ATCCCAAATGATTTTGCTCTGGAGCTTTGCTCCAGATGCTGTTCCC	318			

RESULT 5  
 RAA59061  
 ID AAD59061 standard; cDNA; 1383 BP.  
 AC AAD59061;  
 DT 18-DEC-2003 (first entry)  
 DE Human IRAK4 full length gene #1.

KW Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropin; microbial infection; inflammation; allograft rejection; CIPD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

		OS	Homo sapiens.
		Location/Qualifiers	
FH	key	1..1383	
FT		/*tgc= a	
FT		/product= "Human IRAK4 protein"	
PN	XX	US2003049702-A1.	
XX	PD	13-MAR-2003.	
XX	PP	15-NOV-2001; 2001US-0001254.	
XX	PR	17-NOV-2000; 2000US-00715893.	
XX	PR	17-NOV-2000; 2000US-0367360P.	
XX	PR	29-JUN-2001; 2001US-0301889P.	
PA	(REED/)	REED J. C.	
PA	(GODZ/)	GODZIK A.	
PA	(PAWL/)	PAWLOWSKI K.	
PA	(FIOR/)	FIORENTINO L.	
PA	(LEES/)	LEES S. H.	
PA	(ROTH/)	ROTH W.	
PA	(STEN/)	STENNER-LIWESEN F.	
PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;		
PI	Stenner-Liwezen F;		
XX	XX		
DR	WPI; 2002-5-00322/53.		
DR	P-PSDB; AAE38902.		
XX	XX		
PT	New polypeptide comprising a death domain or death effector domain,		
PT	useful for discovery of drugs that suppress infection, inflammation,		
PT	allergy, sepsis, autoimmunity, allograft rejection and other diseases.		
XX	XX		
PS	Claim 19; Fig 10A; 99pp; English.		
XX	XX		
CC	The present invention provides novel death Domain (DD) and death effector		
CC	domain (DED) proteins and nucleic acids encoding them. The invention also		
CC	provides death domain containing Protein such as Chlamydia trachomatis		
CC	death domain containing protein (CTDD) DD and neural growth factor		
CC	receptor-interacting death domain (NIDD) DD. The invention is useful for		
CC	identifying a binding agent (e.g. protein or drug) that binds a DD, DED		
CC	or NB-ARC domain from DRP3, IRAK4, CINDD, DED4 or NIDD with a candidate		
CC	binding agent and identifying an effective agent (e.g. protein or drug)		
CC	that modulates the association of a DD, DED or NB-ARC domain with protein		
CC	that binds the DD, DED or NB-ARC domain. The invention is also useful for		
CC	modulating the level of cell process such as apoptosis, cell adhesion,		
CC	cell proliferation, cell stress responses, responses to microbial		
CC	infection and B cell immunoglobulin class switching. DB, DBDs and NB-ARC		
CC	useful for discovery of drugs that suppress infection, autoimmunity,		
CC	inflammation, allergy, allograft rejection, sepsis and other diseases.		
CC	DD, DED or NB-ARC domain proteins are used to treat infection, allergy,		
CC	autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte		
CC	hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,		
CC	inflammatory hyperplasia and smooth muscle cell proliferation in arteries		
CC	following balloon angioplasty (restenosis). The invention is also used in		
CC	antibody therapy and gene therapy. The present sequence is human		
CC	interleukin-1 receptor-associated kinase (IRAK)-4 full length gene		
XX	XX		
SO	Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;		
Query Match	100.0%; score 294; DB 6; Length 1383;		
Best Local Similarity	100.0%; Pred. No. 2.3e-77;		
Matches	294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Ov	1 ACTATAGTGGCTCAAGTTGCACTTAATAGGAGCTGTCAATTATGTCCT	60	
Db	25 ACATATGCGCTGCCTCAAGTTGCACTTAATAGGAGCTGTCAATTATGTCCT	84	
Ov	61 CAAAGAAGGATGGAAGAGTAGTGTAGCTATAAAAACATCGGTGATGATAGATC	120	

CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 1668 BP; 571 A; 289 C; 332 G; 476 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 294; DB 5; Length 1668;  
 Best Local Similarity 100.0%; Score 294; DB 5; Length 1668;  
 Matches 294; Conservative 0; Mismatches 0; Pred. No. 2; 4e-77;  
 Db 145 ATCAGTTTCACATAGGAGATTGAGCATTAACCTGGAAAGTCCACTCT 204  
 QY 181 GAATTAATGTTGACTGGGCCACCAATTCGACAGTGTGATCTTGATCTTG 240  
 Db 205 GAATTAATGTTGACTGGGCCACCAATTCGACAGTGTGATCTTGATCTTG 264  
 QY 241 ATCCAAATGATTTTGCCTCTGAGCTTGTCTCCAGATGCGITCCCC 294  
 Db 265 ATCCAAATGATTTTGCCTCTGAGCTTGTCTCCAGATGCGITCCCC 318  
 RESULT 6  
 AAS76805 ID AAS76805 standard; cDNA; 1668 BP.  
 AC AAS76805:  
 XX DT 13-FEB-2002 (first entry)  
 XX DB DNA encoding novel human diagnostic protein #12609.  
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX OS Homo sapiens.  
 PN WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US008631.  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00549167.  
 PA (HYSE-) HYSEQ INC.  
 PI Drmanac RT, Liu C, Tang YT,  
 XX DR WPI; 2001-639362/73.  
 XX DR P-PSDB; ABG12618.  
 XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX PS Claim 1; SEQ ID NO 12609; 103pp; English.  
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tag for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (III). (III) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polyPeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 PN WO200175067-A2.  
 XX PD 22-OCT-2002 (first entry)  
 XX DE Human IRAK4 gene #2.  
 XX KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;  
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;  
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT 50..1432  
 FT /\*tag= a  
 FT /product= "Human IRAK4"  
 PN WO200240680-A2.  
 XX PD 23-MAY-2002.  
 XX PF 15-NOV-2001; 2001WO-US044844.  
 XX PR 17-NOV-2000; 2000US-00715893.  
 PR 29-JUN-2001; 2001US-0301889P.  
 XX PA (BURN-) BURNHAM INST.  
 XX PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,  
 PI Stenner-Liewen F,  
 XX DR WPI; 2002-50222153.  
 XX DR P-PSDB; AAB24865.  
 XX New polypeptide comprising a death domain or death effector domain,  
 PT useful for discovery of drugs that suppress infection, inflammation,  
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

**PS** Claim 19; Page 194-196; 209pp; English.

**XX** The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DP3, IRAK4, CTDP (Chlamydia trachomatis DD protein), DED4 or NRD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent and by Yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDP DD of *C. trachomatis*, *C. muridarum*, *C. pneumoniae* and *C. psittaci* or a nucleic acid encoding the invention is useful for detecting a chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic protein and for proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 gene

**XX** Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other; SQ

Query Match 100.0%; Score 294; DB 6; Length 2817; Best Local Similarity 100.0%; Pred. No. 2.9e-77; Matches 294; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0; QY

DB 74 ACATATGTCGGCTGCCTCATGTGGACTATTAGAAGCTCGAGTTATGATCT 60  
61 CAGAGAGATGAGAGCTTGTGACTATTAACACATCTGGTAGATAGAC 120  
134 CAGAAAGGATGGAGAAGCTTGACTATTAACACATCTGGTAGATAGAC 193

QY 121 ATCAGTTCACTAAGGAGTTGAAGCATCTCAACCTGAAAGTCCACTCT 180  
194 ATACAGTTCACTAAGGAGTTGAAGCATCTCAACCTGAAAGTCCACTCT 253

QY 181 GATTAAGTGTGACTGGGCCAACAAATTCACAGTTGAGATCTTGATCTTG 240  
254 GAATTACTGTGACTGGGCCAACAAATTCACAGTTGAGATCTTGATCTTG 313

Db 241 ATCCAAATATGATTTTGCTCTGCAAGTCTTGTCCAGATGCTGTCCC 294  
314 ATCCAAATATGATTTTGCTCTGCAAGTCTTGTCCCAGATGCTGTCCC 367

**RESULT 8**

AAD59067 ID AAD59067 standard; cDNA; 2817 BP.

AC AAD59067; XX DT 18-DEC-2003 (first entry)

DE Human IRAK4 full length gene #2.

XX DE Human IRAK4 full length gene #2.

XX DE Human IRAK4 full length gene #2.

**KW** keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

**XX** Homo sapiens.

**OS**

**XX**

**FH**

**Key**

**Location/Qualifiers**

**FT** 1..1432 /\*tag= a product "Human IRAK4 protein"

**FT**

**PR** US2003049702-A1.

**PR** 13-MAR-2003.

**PR** 15-NOV-2001; 2001US-00001254.

**PR** 17-NOV-2000; 2000US-00715893.

**PR** 17-NOV-2000; 2000US-0367360P.

**PR** 29-JUN-2001; 2001US-0301889P.

**XX**

**PA** (REED/) REED J C.

**PA** (GODZIK/) GODZIK A.

**PA** (PAWLICKI/) PAWLICKI K.

**PA** (FIORENTINO/) FIORENTINO L.

**PA** (LEESE/) LEE S H.

**PA** (ROTH/) ROTH W.

**PA** (STENNER-LIEWEN/) STENNER-LIEWEN F.

**PI** Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

**XX**

**DR** WPI; 2002-500222/53.

**XX**

**PT** P-PSDB; AAB38906.

**PT** New Polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.

**XX**

**PT** The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein (CTDP) DD and neural growth factor receptor-interacting death domain (NRD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DP3, IRAK4, CTDP, DED4 or NRD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DPs, DEDs and NB-ARC domains and/or anti-DD or anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, that binds the DD, DED or NB-ARC domain. The invention is also useful for cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DPs, DEDs and NB-ARC domains and/or anti-DD or anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human IRAK-4 full length gene

**XX** Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other; SQ

Query Match 100.0%; Score 294; DB 6; Length 2817; Best Local Similarity 100.0%; Pred. No. 2.9e-77; Matches 294; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0; QY

1 ACATATGTCGGCTGCCTCATGTGGACTATTAGAAGCTCGAGTTATGATCT 60  
74 ACATATGTCGGCTGCCTCATGTGGACTATTAGAAGCTCGAGTTATGATCT 133

QY 61 CAAGAAGGATGAGAGACTGTTGACTTAAACCACTCGTGATGATGATAC 120  
 CC (GenBank accession number NM\_016123)  
 XX SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 other;  
 CC Query Match 100.0%; Score 294; DB 10; Length 2817;  
 CC Best Local Similarity 100.0%; Score 294; DB 10; Length 2817;  
 CC Matches 294; Conservative 0; Mi matches 0; Indels 0; Gaps 0;  
 CC Db 194 AACAGTTTCACATAAGGAGTTGAAGCATTAACCTGAAAGTCCACTCT 180  
 CC 121 AACAGTTTCACATAAGGAGTTGAAGCATTAACCTGAAAGTCCACTCT 193  
 CC 194 AACAGTTTCACATAAGGAGTTGAAGCATTAACCTGAAAGTCCACTCT 253  
 QY 181 GAATTACTGTGTTGACTGGGACACAAATTGACAGTGTGATCCTT 240  
 CC 254 GAATTACTGTGTTGACTGGGACACAAATTGACAGTGTGATCCTT 313  
 Db 241 ATCCAATGATTGCTCTGCCTGAGTCTTGTGTCAGATGCTGTTCC 294  
 QY 314 ATCCAATGATTGCTCTGCCTGAGTCTTGTGTCAGATGCTGTTCC 367  
 RESULT 9  
 ACC47548  
 ID ACC47548 standard; DNA; 2817 BP.  
 XX  
 AC ACC47548;  
 XX  
 DT 11-TUL-2003 (first entry)  
 DE Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.  
 KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory;  
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;  
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT  
 FT 50..1432  
 FT /\*tag= a  
 FT /product= "IL-1 receptor-associated kinase-4"  
 XX  
 PN WO2003028636-A2.  
 XX  
 XX 10-APR-2003.  
 XX  
 XX 26-SEP-2002; 2002WO-US030574.  
 XX  
 PR 28-SEP-2001; 2001US-0096451.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Bennett FC; Freier SM;  
 XX PI DR  
 XX DR P-PSDB; ABR44401.  
 XX  
 PT New antisense oligonucleotides for modulating IL-1 receptor-associated  
 PT kinase-4 gene expression, particularly useful for preventing, delaying or  
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an  
 PT infection.  
 XX  
 PS Example 13: Page 80-83; 119PP; English.

The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridising with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridising with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding IL-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The antisense compounds are useful for diagnostics, therapeutics, prophylaxis, or as research reagents or kits. The current sequence represents the human IL-1 receptor-associated kinase-4 encoding sequence

RESULT 9  
 ACC47548  
 ID ACC47548 standard; DNA; 2817 BP.  
 XX  
 AC ACC47548;  
 XX  
 DT 11-TUL-2003 (first entry)  
 DE Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.  
 KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory;  
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;  
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT  
 FT 50..1432  
 FT /\*tag= a  
 FT /product= "IL-1 receptor-associated kinase-4"  
 XX  
 PN WO2003028636-A2.  
 XX  
 XX 10-APR-2003.  
 XX  
 XX 26-SEP-2002; 2002WO-US030574.  
 XX  
 PR 28-SEP-2001; 2001US-0096451.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Bennett FC; Freier SM;  
 XX PI DR  
 XX DR P-PSDB; ABR44401.  
 XX  
 PT New antisense oligonucleotides for modulating IL-1 receptor-associated  
 PT kinase-4 gene expression, particularly useful for preventing, delaying or  
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an  
 PT infection.  
 XX  
 PS Example 13: Page 80-83; 119PP; English.

The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridising with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridising with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding IL-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The antisense compounds are useful for diagnostics, therapeutics, prophylaxis, or as research reagents or kits. The current sequence represents the human IL-1 receptor-associated kinase-4 encoding sequence

RESULT 10  
 AACD10197  
 ID AACD10197 standard; cDNA; 1383 BP.  
 XX  
 AC AACD10197;  
 XX  
 DT 24-SEP-2001 (first entry)  
 XX  
 DE Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.  
 XX  
 Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; IL; antibacterial; antinflammatory; ophthalmological; vasoconstrictive; chronic obstructive pulmonary disease syndrome; pulmonary fibrosis; asthma; ARDS; adult respiratory distress syndrome; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/toll receptor; sarcoidosis; transgenic animal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT  
 FT 1..1383  
 FT /\*tag= a  
 FT /product= "Human IRAK-4"  
 XX  
 PN WO2001151641-A1.  
 XX  
 ED 19-JUL-2001.  
 XX  
 PR 12-JAN-2001; 2001WO-US001171.  
 XX  
 BR 13-JAN-2000; 2000US-0176395P.  
 XX  
 (TULA-) TULARIK INC.  
 XX  
 PI Wesche H, Li S;  
 XX  
 DR WPI; 2001-451860/48.  
 DR P-PSDB; AAE05398.



RESULT 12  
 AADI198  
 ID AADI198 standard; cDNA; 1542 BP.  
 XX  
 AC  
 XX  
 DT 24-SBP-2001 (first entry)  
 XX  
 DE Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.  
 XX  
 MW mouse interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;  
 IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; opd;  
 chronic obstructive pulmonary disease; neuroprotective; chronic cough;  
 adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;  
 interstitial lung disease; allergic rhinitis; transplant rejection;  
 autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;  
 multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;  
 cardiovascular disease; atherosclerosis; neurodegenerative disease;  
 sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;  
 inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;  
 Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/toll receptor;  
 sarcoidosis; transgenic animal; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 PT 1. 1542 /\*tag= a CDS /product= "Mouse IRAK-4"  
 XX  
 PN WO200151641-A1.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PR 12-JAN-2001; 2001WO-US001171.  
 XX  
 PR 13-JAN-2000; 2000US-01176395P.  
 XX  
 PA (TULA-) TULARIK INC.  
 XX  
 PI Wesche H, Li S;  
 DR WPI; 2001-451860/4B.  
 XX  
 DR P-PSDB; AIE05399.  
 XX  
 PS Claim 26; Fig 4; 89pp; English.  
 XX  
 CC The present sequence is a cDNA encoding mouse interleukin (IL)-1 receptor  
 associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and  
 other receptors and act to transduce signals originating from the  
 activated receptors ultimately leading to a variety of downstream  
 effects such as nuclear factor (NF)- $\kappa$ B activation. The IRAK-4  
 inhibitors are useful for treating inflammatory diseases such as  
 pulmonary diseases and diseases of the airway (e.g., adult respiratory  
 disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD),  
 pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or  
 allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,  
 rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or  
 diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),  
 cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of  
 the central nervous system (e.g., neurodegenerative disease), CD14  
 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,  
 psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic  
 dermatitis), inflammatory bowel disease (e.g., Crohn's disease and  
 ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,  
 sarcoidosis and ophthalmic diseases and conditions. The inhibitors of  
 IRAK-4 activity or expression are used to inhibit signal transduction

RESULT 13  
 ACC47549  
 ID ACC47549 standard; DNA; 31000 BP.  
 XX  
 AC  
 XX  
 ACC47549;  
 XX  
 DT 11-JUL-2003 (first entry)  
 XX  
 DE Human DNA complement sequence # SEQ ID 10.  
 XX  
 KW Antisense therapy; cytosolic; antimicrobial; antiinflammatory;  
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;  
 KW disease; infection; diagnostic; therapeutic; prophylaxis;  
 KW  
 OS Homo sapiens.  
 XX  
 DN WO2003028636-A2.  
 XX  
 DD 10-APR-2003.  
 XX  
 PR 26-SBP-2002; 2002WO-US030574.  
 XX  
 PR 28-SBP-2001; 2001US-00966451.  
 XX  
 PR (ISIS) ISIS PHARM INC.  
 XX  
 PR Bennett FC, Freier SM;  
 XX  
 DR WPI; 2003-363356/34.  
 XX  
 PR New antisense oligonucleotides for modulating IL-1 receptor-associated  
 kinase-4 gene expression, particularly useful for preventing, delaying or  
 treating e.g. cancer (e.g. renal cancer), inflammatory disease or an  
 infection.  
 XX  
 PS Example 15; Page 85-102; 119pp; English.

CC resulting from the activation of an interleukin-1 receptor (IL-1R)/toll  
 receptor in a cell. They also inhibit the activation of a transcription  
 factor that activates NFKappaB in the cell. IRAK-4 is used to create a  
 nonhuman transgenic animal which is useful for testing the function of  
 IRAK-4 in vivo, to generate models for the study of inflammatory  
 disorders and conditions and for the development of potential treatments  
 for IRAK-4 related inflammatory diseases and conditions. IRAK-4 sequences  
 are also used in gene therapy and in antisense therapy

Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;

Query Match 69 5%; Score 204 4; DB 5; Length 1542;  
 Best Local Similarity 81.0%; Pred. No. 1.3e-50'; Indels 0; Gaps 0;  
 Matches 238; Conservative 0; Mismatches 56; Gaps 0;

OY	1	ACATGTGCGCTGCCTCAATGTCAGTGGACTAATTAGGAGCTGCGATTATGATCT	60
Db	187	ACATCATCAGCAACCTTAATGTCGGCATCTTGAAGCTGTGGATTTATGATCT	246
OY	61	CAAGAAGGATGAGAAGGAGTAGCTGAGCTATAAAACCATCTGGATGATAGATAC	120
Db	247	CAAGAAGGCTGAGAAGAATAGCAGTAGCTATCAAAGCGTCGGGAGACGATAC	306
OY	121	AATCAGTGTTCATAGGAGAATTGAGCTACTTCAACTGGAAGAACGCCCACCTCT	180
Db	307	ATACAGTCTCCATATAAGGAGTCAGCTTACTTCAGACGGGAGAGCCCAACCTGT	366
OY	181	GAATRACTGTTGACTGGGCCACCAACATGCACTTGCTCCAGATGCTGTCTCC	240
Db	367	GAACTCTGTTGACTGGSCACCCAGAACCTGACAGTGGCACAGTGGACCTGATCTG	426
Db	427	GTCCAGATGAGCTGTTGCCCCACCTCTCCCTGGCGATGCGTCC	480

CC The invention relates to a compound of 8-50 nucleobases which is targeted  
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated  
 CC kinase-4, specifically hybridising with the nucleic acid and inhibiting  
 CC the expression of the encoded product. Also disclosed is the compound  
 CC hybridising with an 8-nucleobase portion of an active site on a nucleic  
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense  
 CC oligonucleotide is useful for treating an animal having a disease or  
 CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer  
 (particularly renal cancer), inflammatory disease or an infection. The  
 CC antisense compounds are useful for diagnostics, therapeutics,  
 CC prophylaxis, or as research reagents or kits. The current sequence is  
 CC utilised in an example from the invention in the design of anti-sense  
 CC oligonucleotides, and represents the complement of the human DNA sequence  
 XX that is given as Genbank accession number AC016143

SQ Sequence 31000 BP; 9247 A; 5056 C; 5924 G; 9973 T; 0 U; 0 Other;  
 Query Match 51.6%; Score 151.8; DB 10; Length 31000;  
 Best Local Similarity 95.7%; Pred. No. 1.7e-34; Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Ov 123 TCAGTTTCACTAAGGAGATGTGAACTACTTCAACTGGAAAAGTCCACTTCGA 182  
 Db 12953 TTACTTACCTTAAGGAGATTTGAGCATTTACTCAACAGGGAAAAGTCCACTTCGA 13012  
 Ov 183 ATTAATGTTGACTGGGCCAACATTGACAGTTGGATCTTGACGTTTGTAT 242  
 Db 13013 ATTACTGTGTTGACTGGGCCAACATTGACAGTTGGATCTTGACGTTTGTAT 13072  
 Ov 243 CCAAATGAAATTGCTCGAGCTTGTCCAGAT 285  
 Db 13073 CCAAATGAAATTGCTCGAGCTTGTCCAGAT 13115

RESULT 14

ID AAS7603 standard; cDNA; 405 BP.  
 XX AAS7603;  
 AC  
 XX  
 DT 13-FEB-2002 (first entry)  
 DE DNA encoding novel human diagnostic protein #12607.  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.

RESULT 15

ID AAD40084 standard; DNA; 211 BP.  
 XX AAD40084;  
 AC  
 DT 22-OCT-2002 (first entry)  
 DE Human IRAK4 short gene.  
 KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;  
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;  
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.  
 OS Homo sapiens.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX DR WPI, 2001-639362/73.  
 DR P-PSDB; ABQ12616.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX  
 PS Claim 1; SEQ ID NO 12607; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS4197-AAS4564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/publish\_pct\_sequences

SQ Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;  
 Query Match 51.2%; Score 150.4; DB 5; Length 405;  
 Best Local Similarity 99.3%; Pred. No. 1e-34; Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Ov 134 TAAGGAGTTGAGCATTTACTCAAACTGGAAAAGTCCACTCTGAAATTGTTG 193  
 Db 115 TAAGGAGTTGAGCATTTACTCAAACTGGAAAAGTCCACTCTGAAATTGTTG 174  
 Ov 194 ACTGGGCCACCAAAATGACAGTTGTAATCTGTGATCTTGATGCCAAATGAT 253  
 Db 175 ACTGGGCCACCAAAATGACAGTTGTAATCTGTGATCTTGATGCCAAATGAT 234  
 Ov 254 TTTTGCTCCCTCGAGCTTGTGTCCTCAGAT 285  
 Db 235 TTTCGCTCCCTCGAGCTTGTGTCCTCAGAT 266

RESULT 16

ID AAD40084 standard; DNA; 211 BP.  
 XX AAD40084;  
 AC  
 DT 22-OCT-2002 (first entry)  
 DE Human IRAK4 short gene.  
 KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;  
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;  
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.  
 OS Homo sapiens.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX DR WPI, 2001-639362/73.  
 DR P-PSDB; ABQ12616.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX  
 PS Claim 1; SEQ ID NO 12607; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS4197-AAS4564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/publish\_pct\_sequences

SQ Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;  
 Query Match 51.2%; Score 150.4; DB 5; Length 405;  
 Best Local Similarity 99.3%; Pred. No. 1e-34; Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Ov 134 TAAGGAGTTGAGCATTTACTCAAACTGGAAAAGTCCACTCTGAAATTGTTG 193  
 Db 115 TAAGGAGTTGAGCATTTACTCAAACTGGAAAAGTCCACTCTGAAATTGTTG 174  
 Ov 194 ACTGGGCCACCAAAATGACAGTTGTAATCTGTGATCTTGATGCCAAATGAT 253  
 Db 175 ACTGGGCCACCAAAATGACAGTTGTAATCTGTGATCTTGATGCCAAATGAT 234  
 Ov 254 TTTTGCTCCCTCGAGCTTGTGTCCTCAGAT 285  
 Db 235 TTTCGCTCCCTCGAGCTTGTGTCCTCAGAT 266

PA (BURN-) BURNHAM INST.

XX

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PT Steiner-Liewen F;

XX

WPI; 2002-50022/53.

DR P-FSDB; RAB24864.

XX

PT New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX

PS Claim 19; Page 195; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell.

CC Antibody specifically reactive with CTDD DD of C. trachomatis , C. muridarum, C. pneumoniae and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 short gene

SQ Sequence 211 BP; 77 A; 41 C; 36 G; 57 T; 0 U; 0 Other;

Query Match 46.8%; Score 137.6; DB 6; Length 211;  
Best Local Similarity 97.2%; Pred. No. 5.5e-31; Mismatches 140; Conservative 0; MisMatches 4; Indels 0; Gaps 0;

QY	1	ACATATGTCGGCTGCCTCAATGTTGACTATTAGAAAGCTGTGATTTATGATCCT	60
	25	ACATATGTCGGCTGCCTCAATGTTGACTATTAGAAAGCTGTGATTTATGATCCT	84
QY	61	CAAGGAGGATGAGAAGTGTGCTTAGTATAAACCATCTGGATGATGATAC	120
Db	85	CAAGGAGGATGAGAAGTGTGCTTAGTATAAACCATCTGGATGATGATAC	144
QY	121	ATCAGTTCAATAGGAGTT	144
Db	145	ATCAGTTCAATAGTGT	168



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Gencore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:29:43 ; Search time 1843 Seconds  
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Searched:	4526729 seqs, 2364484745 residues
Total number of hits satisfying chosen parameters:	9053458
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Post-processing:	Minimum Match 0%

21 204.4 69.5 2431 10 BC051676 EC051576 Mus muscu  
 22 151.8 51.6 31000 6 AR47555 Sequence AR47555 Mus muscu  
 23 151.8 33033 9 AY186092 Homo sapi  
 24 151.8 51.6 118572 9 AC093012 Homo sapi  
 25 151.8 51.6 165868 2 AC021719 Homo Bapi  
 C 26 151.8 51.6 309582 2 AC025567 Homo sapi  
 AX313115 Sequence  
 CQ81170 Sequence  
 AY40964 Homo sapi  
 AX340955 Homo sapi  
 AK027301 Homo Bapi  
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 BD155790 Primer fo  
 AC12390 Rattus no  
 AC147160 Mus muscu  
 AY61654 Danio rer  
 BC045381 Danio rer.  
 AC123081 Rattus no  
 AC094859 Rattus no  
 BV075713 S212P6044 Continuation (4 of  
 C 40 54.2 18.9 756 11 AC134788\_3 Continuation (2 of  
 C 41 46.8 98858 2 AC03663\_1 AE010646 Fusobacte  
 C 42 46.8 15.9 11000 2 AE010646 Fusobacte  
 C 43 43.4 14.6 9990 1 BV034947 S212P6037  
 C 44 42.8 14.6 574 1 BV034947 S212P6037  
 C 45 42.6 14.5 1691 6 CQ719522 Sequence

**QY** 121 ATTCAGTTACATAAGGAGATTGAGACATTACTCAACTGGAAAAGTCCACTCT 180  
**Db** 121 AATCAGTTACATAAGGAGATTGAGACATTACTCAACTGGAAAAGTCCACTCT 180  
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**SOURCE**  
**QY** 181 GAATTACTGTGTGACTGGGCCACCAAAATGCACAGTTGATCTTGATGATCTT 240  
**Db** 181 GAATTACTGTGTGACTGGGCCACCAAAATGCACAGTTGATCTTGATGATCTT 240  
**FEATURES**  
**SOURCE**  
**QY** 241 ATCCAAATGATTTTGCTCTCGAGCTTCTCCAGAGCTGTCCC 294  
**Db** 241 ATCCAAATGATTTTGCTCTCGAGCTTCTCCAGAGCTGTCCC 294  
**CDS**  
**ORIGIN**  
**REFERENCE**  
**AUTHORS** Scianian, M.J., Stockert, E., Chen, Y.-T., Old, L.J., Jager, E. and Knuth, A.  
**TITLE** Renal cancer associated antigens and uses therefor  
**JOURNAL** Patent: US 644063-A 10 27-AUG-2002;  
**FEATURES** location/Qualifiers  
**Source** 1..833  
*/organism="unknown"*  
*/mol\_type="genomic DNA"*

**ORIGIN**  
**REFERENCE**  
**AUTHORS** Best Local Similarity 100.0%; Score 294; DB 6; Length 833; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**QY** 1 ACATATGCGCCGCTCATGTTGACTATAGGAAGCTGTCAGATTATGATCT 60  
**Db** 74 ACATATGCGCCGCTCATGTTGACTATAGGAAGCTGTCAGATTATGATCT 133  
**QY** 61 CAGAAGGATGGAGAAGTTGCTGAGCTTAAACACATCTGGTGTAGATAC 120  
**Db** 134 CAGAAGGATGGAGAAGTTGCTGAGCTTAAACACATCTGGTGTAGATAC 193  
**QY** 121 ATTCAGTTACATAAGGAGATTGAGACATTCTCAAATCGAAAAGTCCACTCT 180  
**Db** 194 ATTCAGTTACATAAGGAGATTGAGACATTCTCAAATCGAAAAGTCCACTCT 253  
**QY** 181 GAATTACTGTGTGACTGGGCCACCAAAATGCACAGTTGATCTTGATGATCTT 240  
**Db** 254 GAATTACTGTGTGACTGGGCCACCAAAATGCACAGTTGATCTTGATGATCTT 313  
**QY** 241 ATCCAAATGATTTTGCTCTCGAGCTTCTCCAGAGCTGTCCC 294  
**Db** 314 ATCCAAATGATTTTGCTCTCGAGCTTCTCCAGAGCTGTCCC 367

---

**RESULT 3**  
**AX431306**  
**LOCUS** AX431305  
**DEFINITION** Sequence 15 from Patent WO2002040680.  
**ACCESSION** AX431306  
**VERSION** AX431305.1  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 1636)  
**AUTHORS** Chuang, T.H. and Ulevitch, R.J.  
**TITLE** Human interleukin-1 receptor associated kinase 4 cDNA sequences  
**JOURNAL** Unpublished  
**FEATURES**  
**AUTHORS** Chuang, T.H. and Ulevitch, R.J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (14-JUL-2003) Immunology, The Scripps Research Institute, 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA  
**FEATURES** source  
*1..1636*

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**RESULT 2**  
**AR223870**  
**LOCUS** AR223870  
**DEFINITION** Sequence 10 from patent US 644063. DNA linear PAT 26-SEP-2002  
**ACCESSION** AR223870  
**VERSION** AR223870.1  
**KEYWORDS** Unknown  
**ORGANISM** Unclassified  
**REFERENCE**  
**AUTHORS** Scianian, M.J., Stockert, E., Chen, Y.-T., Old, L.J., Jager, E. and Knuth, A.  
**TITLE** Renal cancer associated antigens and uses therefor  
**JOURNAL** Patent: US 644063-A 10 27-AUG-2002;  
**FEATURES** location/Qualifiers  
**Source** 1 (bases 1 to 833)  
*/organism="unknown"*  
*/mol\_type="genomic DNA"*

**ORIGIN**  
**REFERENCE**  
**AUTHORS** Best Local Similarity 100.0%; Score 294; DB 6; Length 1383; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**QY** 1 ACATATGCGCCGCTCATGTTGACTATAGGAAGCTGTCAGATTATGATCT 60  
**Db** 25 ACATATGCGCCGCTCATGTTGACTATAGGAAGCTGTCAGATTATGATCT 84  
**QY** 61 CAGAAGGATGGAGAAGTTGCTGAGCTTAAACACATCTGGTGTAGATAC 120  
**Db** 85 CAGAAGGATGGAGAAGTTGCTGAGCTTAAACACATCTGGTGTAGATAC 144  
**Db** 145 AATCAGTTACATAAGGAGATTGAGACATTCTCAAATCGAAAAGTCCACTCT 180  
**QY** 121 ATTCAGTTACATAAGGAGATTGAGACATTCTCAAATCGAAAAGTCCACTCT 180  
**Db** 204 ATTCAGTTACATAAGGAGATTGAGACATTCTCAAATCGAAAAGTCCACTCT 204  
**QY** 181 GAATTACTGTGTGACTGGGCCACCAAAATGCACAGTTGATCTTGATGATCTT 240  
**Db** 205 GAATTACTGTGTGACTGGGCCACCAAAATGCACAGTTGATCTTGATGATCTT 264  
**QY** 241 ATCCAAATGATTTTGCTCTCGAGCTTCTCCAGAGCTGTCCC 294  
**Db** 265 ATCCAAATGATTTTGCTCTCGAGCTTCTCCAGAGCTGTCCC 318

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**RESULT 4**  
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**LOCUS** AY340962  
**DEFINITION** Homo sapiens interleukin-1 receptor-associated kinase 4 (IRAK4) mRNA, complete cds; alternatively spliced.  
**ACCESSION** AY340962  
**VERSION** AY340962.1  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 1636)  
**AUTHORS** Chuang, T.H. and Ulevitch, R.J.  
**TITLE** Human interleukin-1 receptor associated kinase 4 cDNA sequences  
**JOURNAL** Unpublished  
**FEATURES**  
**AUTHORS** Chuang, T.H. and Ulevitch, R.J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (14-JUL-2003) Immunology, The Scripps Research Institute, 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA  
**FEATURES** source  
*1..1636*

1. .1684

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/db\_xref="taxon:606"

/chromosome="12"

/map="12q12"

/tissue\_type="spleen"

1. .1636

/gene="IRAK4"

/note="IRAK4; protein kinase; alternatively spliced"

/product="interleukin-1 receptor-associated kinase 4"

/protein\_id="P402358\_1"

/db\_xref="GI:37727959"

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SPTRFHSFSPYLKVNTNFDERPISGUNGNKGGBGGFVVYKGVYNTTVWAKLAM

VDTTEBLKQDFQKOMPKACOHHENLVLGEPSDGDICLUVVWMPNGSLDRSC

LQGTPPSWHMCKIACDGAANGNHLRDKSANTLIDBAPTAKSDFGILAR

ASERKQTMTSRIVGTYAMAPRLRGITKSDIVSGVULITGLPVADEIRE

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QOLQEMTAS"

ORIGIN

Query Match 100.0%; Score 294; DB 9; Length 1636;

Best Local Similarity 100.0%; Pred. No. 1.7e-64; Mismatches 0; Indels 0; Gaps 0;

Matches 294; Conservative 0; MisMatches 0; Variant 1

1 ACATATGCGCTGCCTCAATGTCAGTGGACTTATTAGAACCTGCTGAGATTTATGATCT 60

90 ACATATGCGCTGCCTCAATGTCAGTGGACTTATTAGAACCTGCTGAGATTTATGATCT 149

61 CAAAGAGGATGGAAGAGTGGTAGCTGTAGTAAACCATCTGGTAGATAC 120

150 CAAAGAGGATGGAAGAGTGGTAGCTGTAGTAAACCATCTGGTAGATAC 209

121 AATCAGTTTCACATAGGAGATTAAGCATTAATCTTCACAGTGTTCTGACTCT 180

210 AATCAGTTTCACATAGGAGATTAAGCATTAATCTTCACAGTGTTCTGACTCT 269

181 GAATTACTGTGACTGGCCACCAATTCGCAAGTGTTCTGACTCT 240

270 GAATTACTGTGACTGGCCACCAATTCGCAAGTGTTCTGACTCT 329

241 ATCCAATGATTITGCTCTGGAGCTTGTCTCCAGATGCTTTCCC 294

330 ATCCAATGATTITGCTCTGGAGCTTGTCTCCAGATGCTTTCCC 383

ORIGIN

Query Match 100.0%; Score 294; DB 9; Length 1684;

Best Local Similarity 100.0%; Pred. No. 1.7e-64; Mismatches 0; Indels 0; Gaps 0;

Matches 294; Conservative 0; MisMatches 0; Variant 1

1 ACATATGCGCTGCCTCAATGTCAGTGGACTTATTAGAACCTGCTGAGATTTATGATCT 60

138 ACATATGCGCTGCCTCAATGTCAGTGGACTTATTAGAACCTGCTGAGATTTATGATCT 197

61 CAAAGAGGATGGAAGAGTGGTAGCTGTAGTAAACCATCTGGTAGATAC 120

198 CAAAGAGGATGGAAGAGTGGTAGCTGTAGTAAACCATCTGGTAGATAC 257

121 AATCAGTTTCACATAGGAGATTAAGCATTAATCTTCACAGTGTTCTGACTCT 180

258 AATCAGTTTCACATAGGAGATTAAGCATTAATCTTCACAGTGTTCTGACTCT 317.

181 GAATTACTGTGACTGGCCACCAATTCGCAAGTGTTCTGACTCT 240

318 GAATTACTGTGACTGGCCACCAATTCGCAAGTGTTCTGACTCT 377

241 ATCCAATGATTITGCTCTGGAGCTTGTCTCCAGATGCTTTCCC 294

378 ATCCAATGATTITGCTCTGGAGCTTGTCTCCAGATGCTTTCCC 431

RESULT 5

AJ340963

LOCUS AY340963

DEFINITION Homo sapiens interleukin-1 receptor-associated kinase 4 variant (IRAK4) mRNA, complete cds; alternatively spliced.

ACCESSION AY340963

VERSION 1

KEYWORDS GI:37727960

SOURCE

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1684)

AUTHORS Chuang,T.H. and Ulevitch,R.J.

TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1684)

AUTHORS Chuang,T.H. and Ulevitch,R.J.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute, 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA

FEATURES location/Qualifiers

RESULT 6

CQ728380

LOCUS CQ728380

DEFINITION Sequence 14314 from Patent WO20068579.

ACCESSION CQ728380

VERSION CQ728380.1

KEYWORDS GI:42297030

SOURCE

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 14314 06-SEP-2002;

FEATURES location/Qualifiers

source 1. .2775

Db 314 ATCCAAATGAATTTCGCTCTGGAGCTTGTCCCAGATCTGTCCC 367

ORIGIN /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606"

Query Match Best Local Similarity 100.0%; Score 294; DB 6; Length 2775; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGCGCTGCCTCAACTTGACTTAATGGAGCTGTCAGTTATTGATCT 60

Db 36 ACATATGCGCTGCCTCAACTTGACTTAATGGAGCTGTCAGTTATTGATCT 95

Qy 61 CAAGAGGATGGAAGAAGTAGCTGACTTAAACCATCGTGTGATGATAC 120

Db 96 CAAGAGGATGGAAGAAGTAGCTGACTTAAACCATCGTGTGATGATAC 155

Qy 121 ATCAGTTTCACATAGGAGATTGAGCTTAAACCATCGTGTGATGATAC 180

Db 156 AATCAGTTTCACATAGGAGATTGAGCTTAAACCATCGTGTGATGATAC 215

Qy 181 GAATTAATGTTGACTGGGCCACCAAAATTGACAGTGGTGTCTTGACTCT 240

Db 216 GAATTAATGTTGACTGGGCCACCAAAATTGACAGTGGTGTCTTGACTCT 275

Qy 241 ATCCAAATGAATTTCGCTCTGGAGCTTGTCCCAGATCTGTCCC 294

Db 276 ATCCAAATGAATTTCGCTCTGGAGCTTGTCCCAGATCTGTCCC 329

RESULT 7 AR475548

LOCUS AR475548 DEFINITION Sequence 3 from patent US 6692959. DNA LINEAR PAT 20-FEB-2004

ACCESSION AR475548 VERSION AR475548.1

KEYWORDS Unknown.

SOURCE Unclassified.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2817)

AUTHORS Bennett,C.F. and Freier,S.M.

TITLE Antisense modulation of IL-1 receptor-associated kinase-4 expression

JOURNAL Patent: US 6692959-A 3 17-FEB-2004;

FEATURES Source 1..2817 /organism="unknown" /mol\_type="genomic DNA"

ORIGIN /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606" /note="unnamed protein product" /codon\_start=1 /protein\_id=CAD37285\_1" /db\_xref="GI:21656188" /translation="MKEITPSIVRCLAVLJKRSDFIDPQEGKKLAWIKKPSG DAVRTANTLPSKELAIVQQKOMPCDKDRUMTPYONLSDPSSMPDSEESLVE DVIDTEBKQOFOBIEKMKQKCSANTILDAFTAKSLPQLDIDKREIEDEEKTIEDYIDKMDADSISVEMYSGASQCRCHEKKNQSPDIKV HQLQEMTAS"

Query Match Best Local Similarity 100.0%; Score 294; DB 6; Length 2817; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGCGCTGCCTCAACTTGACTTAATGGAGCTGTCAGTTATTGATCT 60

Db 74 ACATATGCGCTGCCTCAACTTGACTTAATGGAGCTGTCAGTTATTGATCT 133

Qy 61 CAAGAGGATGGAAGAAGTAGCTGACTTAAACCATCGTGTGATGATAC 120

Db 134 CAAGAGGATGGAAGAAGTAGCTGACTTAAACCATCGTGTGATGATAC 193

Qy 121 ATCAGTTTCACATAGGAGATTGAGCTTAAACCATCGTGTGATGATAC 180

Db 194 ATCAGTTTCACATAGGAGATTGAGCTTAAACCATCGTGTGATGATAC 253

Qy 181 GAATTAATGTTGACTGGGCCACCAAAATTGACAGTGGTGTCTTGACTCT 240

Db 254 GAATTAATGTTGACTGGGCCACCAAAATTGACAGTGGTGTCTTGACTCT 313

Db 241 ATCCAAATGAATTTCGCTCTGGAGCTTGTCCCAGATCTGTCCC 294

Db 314 ATCCAAATGAATTTCGCTCTGGAGCTTGTCCCAGATCTGTCCC 367

RESULT 9 AF155118

LOCUS AF155118 DEFINITION Homo sapiens putative protein kinase NY-REN-64 antigen mRNA, complete cds.

ACCESSION AF155118 VERSION AF155118.1 GI:5360130

KEYWORDS	ACCESSION
SOURCE	AK000528
ORGANISM	Homo sapiens (human)
Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Cattarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 2817)
AUTHORS	Scanlan,M.J., Gordan,J.D., Williamson,B., Stockert,B., Bander,N.H., Jongenel,V., Gure,A.O., Jager,D., Jager,B., Knuth,A., Chen,Y.-T.
TITLE	Antigens recognized by autologous antibody in patients with renal-cell carcinoma
JOURNAL	Int. J. Cancer 83 (4), 456-464 (1999)
MEDLINE	99438124
PUBLMED	10508479
REFERENCE	2 (bases 1 to 2817)
AUTHORS	Scanlan,M.J., Gordan,J.D., Williamson,B., Stockert,B., Bander,N.H., Jongenel,V., Gure,A.O., Jager,D., Jager,B., Knuth,A., Chen,Y.-T.
TITLE	Direct Submission
JOURNAL	Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA
FEATURES	Location/Qualifiers
source	1. .2817 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="1973:10-4" /cell_type="renal cell carcinoma" 50. .1-32
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ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 1.6e-64;
Matches	294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	74 ACATATGTCGGCTCGCTCAATGTTGACTTAATTAGAACCTGCGATTTATGATCT
Qy	61 CAAGAGGAGATGGAAAGTAGTTGACTGTTAGTATAAAACCATCTGGATGATAGATAC
Db	134 CAAGAGGAGATGGAAAGTAGTTGACTGTTAGTATAAAACCATCTGGATGATAGATAC
Qy	121 ATCAGTTCACATAGGAGATTCAGATTAATCTCAAACTGAAAGTCCACTCT
Db	194 ATCAGTTCACATAGGAGATTCAGATTAATCTCAAACTGAAAGTCCACTCT
Qy	181 GAATTAATGTTGACTGGGACACCAAACTGCAAGTTGAGCTTGATCTTGATCTTGC 240
Db	254 GAATTAATGTTGACTGGGACACCAAACTGCAAGTTGAGCTTGATCTTGATCTTGC 313
Qy	241 ATCCAAATGATTITGCTCTGGAGTTGCTCCAGATGCTGTTCCC 294
Db	314 ATCCAAATGATTITGCTCTGGAGTTGCTCCAGATGCTGTTCCC 367
RESULT	10 AK000528
DEFINITION	Homo sapiens cDNA FLJ20521 fis, clone KAT10395.
Locus	AK000528 2820 bp mRNA linear PRI 13-SEP-2003
KEYWORDS	ACCESSION
SOURCE	AK000528.1 GI:7020693
VERSION	oligo capping; fis (full insert sequence).
KEYWORDS	
SOURCE	
ORGANISM	
Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Cattarrhini; Hominidae; Homo.	
REFERENCE	1
AUTHORS	Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE	NEDO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2820)
AUTHORS	Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE	Direct Submission
JOURNAL	Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:f1cdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5' & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
FEATURES	Location/Qualifiers
source	1. .2820 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="KAT1035" /cell_line="KATO III" /cell_type="signet-ring cell carcinoma" /clone_id="KAT" /note="cloning vector pME18SFL3" 30. .-1412 /note="unnamed protein product" /codon_start=1 /protein_id="BA91232.1" /db_xref="31: 7020694"
CDS	
ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 1.6e-64;
Matches	294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ACATATGTCGGCTCGCTCAATGTTGACTTAATTAGAACCTGCGATTTATGATCT
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Qy	61 CAAGAGGAGATGGAAAGTAGTTGACTGTTAGTATAAAACCATCTGGATGATAGATAC
Db	134 CAAGAGGAGATGGAAAGTAGTTGACTGTTAGTATAAAACCATCTGGATGATAGATAC
Qy	121 ATCAGTTCACATAGGAGATTCAGATTAATCTCAAACTGAAAGTCCACTCT
Db	194 ATCAGTTCACATAGGAGATTCAGATTAATCTCAAACTGAAAGTCCACTCT
Qy	181 GAATTAATGTTGACTGGGACACCAAACTGCAAGTTGAGCTTGATCTTGATCTTGC 240
Db	254 GAATTAATGTTGACTGGGACACCAAACTGCAAGTTGAGCTTGATCTTGATCTTGC 313
Qy	241 ATCCAAATGATTITGCTCTGGAGTTGCTCCAGATGCTGTTCCC 294
Db	314 ATCCAAATGATTITGCTCTGGAGTTGCTCCAGATGCTGTTCCC 367
RESULT	10 AK000528
DEFINITION	Homo sapiens cDNA FLJ20521 fis, clone KAT10395.
Locus	AK000528 2820 bp mRNA linear PRI 13-SEP-2003

QY 241 ATCCAAATGAAATTTCCTCGCGAGCTTGTGCTCCAGATGCTGTCCC 294  
Db 294 ATCCAAATGAAATTTCCTCGCGAGCTTGTGCTCCAGATGCTGTCCC 347

RESULT 11  
AY283671 LOCUS AY283671  
DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 mutant form 2 (IRAK4) mRNA, complete cds.  
ACCESSION AY283671  
VERSION AY283671.1  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
JOURNAL J. Exp. Med. (2003) In press  
REFERENCE 1. (bases 1 to 1381)  
AUTHORS Medvedev,A.E., Lentsch.A., Kuhns,D.B., Blanco,J.C.G.,  
Sakowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.  
TITLE Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections  
JOURNAL Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA  
FEATURES source

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/db\_xref="Laxon:9606"  
/db\_xref=".1381"  
/organism="Homo sapiens"  
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/product="interleukin-1 receptor associated kinase 4"  
/protein\_form="2"  
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/db\_xref="GI:31871820"  
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variation  
ORIGIN

Query Match 99.5%; Score 292.4; DB 9; Length 1381;  
Best Local Similarity 99.7%; Pred. No. 4; 3e-64;  
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCCTCAATGTGGACTAATTAGGAGCTGTCAGATTATGATCT 60  
Db 25 ACATATGTCGCTGCCTCAATGTGGACTAATTAGGAGCTGTCAGATTATGATCT 84

QY 61 CAAGAGGAGTAGGAGAGATGAGATTAGCTGAGCTTAATTAACACATCTGGATGATAC 120  
Db 85 CAAGAGGAGTAGGAGAGATGAGATTAGCTGAGCTTAATTAACACATCTGGATGATAC 144

QY 121 AACATGTTCACTAACATAGGAGATGAGATTAGCTGAGCTTAATTAACACATCTGGATGATCT 180  
Db 145 AACATGTTCACTAACATAGGAGATGAGATTAGCTGAGCTTAATTAACACATCTGGATGATCT 204

QY 181 GAATTAATGTTGACTGGCACACAAATGAGCTGTCAGTTGATCTGTGATCCTTG 240  
Db 205 GAATTAATGTTGACTGGCACACAAATGAGCTGTCAGTTGATCTGTGATCCTTG 264

QY 241 ATCCAAATGAAATTTCCTCGCGAGCTTGTGCTCCAGATGCTGTCCC 294

QY 121 AACATGTTCACTAACATAGGAGATGAGATTAGCTGAGCTTAATTAACACATCTGGATGATCT 180  
Db 145 AACATGTTCACTAACATAGGAGATGAGATTAGCTGAGCTTAATTAACACATCTGGATGATCT 204

QY 181 GAATTAATGTTGACTGGCACACAAATGAGCTGTCAGTTGATCTGTGATCCTTG 240  
Db 205 GAATTAATGTTGACTGGCACACAAATGAGCTGTCAGTTGATCTGTGATCCTTG 264

Db	265	ATCCAAATGATTTCCTCGAGCTTGTCTCCAGATGCTTCCC 318	OY	121 AATCAGTTCACTAAGGGATTTGACCATCTCAACTGGAAAGTCACACTCT 180
RESULT	13		Db	145 ATCAGTTCACTAAGGGATTTGACCATCTCAACTGGAAAGTCACACTCT 204
LOCUS	AF445802	1383 bp mRNA linear PRI 20-APR-2002	OY	181 GAATTAATCTTGACTGGGCACCAAAATTGACAGTGGTCACTTGTGGAATCTTG 240
DEFINITION	Homo sapiens interleukin-1 receptor associated kinase 4 (IRAK4)	mRNA, complete cds.	Db	205 GAATTAATCTTGACTGGGCACCAAAATTGACAGTGGTCACTTGTGGAATCTTG 264
ACCESSION	AF445802		OY	241 ATCCAAATGATTTCCTCGAGCTTGTCTCCAGATGCTTCCC 294
VERSION	AF445802.1	GI:20219009	Db	265 ATCCAAATGATTTCCTCGAGCTTGTCTCCAGATGCTTCCC 318
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1. (bases 1 to 1383)		RESULT	14
AUTHORS	Li,S., Strulov,A., Fontana,E.J. and Wesche,H.		AY83670	AY83670
TITLE	IRAK-4: a novel member of the IRAK family with the properties of an IRAK-kinase		LOCUS	AY83670
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (8), 5567-5572 (2002)		DEFINITION	Homo sapiens interleukin-1 receptor associated kinase 4 mutant form 1 (IRAK4) mRNA, complete cds.
MEDLINE	2195277		ACCESSION	AY83670
PUBMED	11960013		VERSION	AY83670.1 GI:31871817
REFERENCE	2. (bases 1 to 1383)		KWOWDWS	
AUTHORS	Suzuki,N., Suzuki,S., Duncan,G.S., Millar,D.G., Wada,T., Mirtsois,C., Takada,H., Wakeham,A., Itie,A., Li,S., Penninger,J.M., Wesche,H., Ohashi,P.S., Mak,T.W. and Yeh,W.C.		SOURCE	Homo sapiens (human)
TITLE	Severe impairment of interleukin-1 and Toll-like receptor signalling in mice lacking IRAK-4		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	Nature 416 (6882), 750-756 (2002)		REFERENCE	1. (bases 1 to 1383)
MEDLINE	21953195		AUTHORS	Medvedev,A.B., Lentchach,A., Kuhne,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
PUBMED	11923871		TITLE	Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
REFERENCE	3. (bases 1 to 1383)		JOURNAL	J. Exp. Med. (2003) In press
AUTHORS	Li,S., Strelow,A., Fontana,E.J. and Wesche,H.		AUTHORS	Medvedev,A.B., Lentchach,A., Kuhne,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
TITLE	Direct Submission		TITLE	Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
JOURNAL	Submitted (08-NOV-2001) Biology I, Tularik Inc., 2 Corporate Drive, South San Francisco, CA 94080, USA		JOURNAL	J. Exp. Med. (2003) In press
FEATURES	source		AUTHORS	Medvedev,A.B., Lentchach,A., Kuhne,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
gene	/organism="Homo sapiens"		TITLE	Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
CDS	/mol_type="mRNA"		JOURNAL	Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA
gene	/db_xref="taxon:9606"		FEATURES	source
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	/gene="IRAK4"		/organism="Homo sapiens"	
	1. .1383		/mol_type="mRNA"	
	/gene="IRAK4"		/isolation="patient hyporesponsive to lipopolysaccharide and interleukin-1 and suffering from recurrent bacterial infections"	
	/note="protein kinase"		/db_xref="taxon:9606"	
	/codon_start=1		/note="genotype: compound heterozygous"	
	/product="interleukin-1 receptor associated kinase 4"		1. .1383	
	/protein_id=AAU15772.1		/gene="IRAK4"	
	/db_xref="GI:20219010"		1. .879	
	/translation="MNKPITPTPYCLVNLGLRKLSDFIDPQEGMKLAVAIKKSG DRYNQHPIRRLAELQFQSPISLFLFDWGTTNCYAGDLVNLQNEFFAPASLLP DTRPFHRSFVYLKVNTNFDRPSVGGNGEFGFGVVKGVNTVAVKKLAM VDTTEBKQDQDCKIKAQMKQHNLVNLVFLGFSDDCLIVVYVMPNGSLDRSC LDGTPPLSWHMECKIAQGAANGINHHLHRDANSILDEBARTAKISDFGIGAR ASEKFAQTMPSVITGTYMAPELRGEITKSYDISPGVLUETLGIPAVDEIRE PQLLDRKEBEDEKTIEDYIDKMDADSTSVSEAMSVASQCILHEKKNPKDICKV QQLIQEMTAS"			
ORIGIN			/codon_start=1	
Query Match	99.5%; Score 292.4; DB 9; Length 1383;		/product="interleukin-1 receptor associated kinase 4"	
Best Local Similarity	99.7%; Pred No. 4.3e-64; Mismatches 1; Indels 0; Gaps 0;		/mutant_form "1"	
Matches	293; Conservative 0; MisMatches 1;		/protein_id="AAD57089.1"	
OY	1 ACATATGTCGCCGCTCAATGTTGACTTATGGAGCTGCAATTGATCT 60		/db_xref="GI:31871818"	
Db	25 ACATATGTCGCCGCTCAATGTTGACTTATGGAGCTGCAATTGATCT 84		/translation="MNKPITPTPYCLVNLGLRKLSDFIDPQEGMKLAVAIKKSG DRYNQHPIRRLAELQFQSPISLFLFDWGTTNCYAGDLVNLQNEFFAPASLLP DTRPFHRSFVYLKVNTNFDRPSVGGNGEFGFGVVKGVNTVAVKKLAM VDTTEBKQDQDCKIKAQMKQHNLVNLVFLGFSDDCLIVVYVMPNGSLDRSC LDGTPPLSWHMECKIAQGAANGINHHLHRDANSILDEBARTAKISDFGIGAR ASEKFAQTMPSVITGTYMAPELRGEITKSYDISPGVLUETLGIPAVDEIRE PQLLDRKEBEDEKTIEDYIDKMDADSTSVSEAMSVASQCILHEKKNPKDICKV QQLIQEMTAS"	
OY	61 CAAGAGGATGGAAGAGTAGCTGTAGTAAACATCTGGTGTAGATAGATC 120		/gene="IRAK4"	
Db	85 CAAGAGGATGGAAGAGTAGCTGTAGTAAACATCTGGTGTAGATAGATC 144		/note="site of mutation 1; replacement results in premature stop codon to glutamine amino acid change; as compared to GenBank Accession Number AY83671 and wild-type IRAK4"	
			/replace="C"	

## ORIGIN

Query Match 99.5%; Score 292.4; DB 9; Length 1383;

Best Local Similarity 99.7%; Pred. No. 4.3e-64; Mismatches 0; Indels 0; Gaps 0;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACATATGTCGCGCTGCCATAGTGGACTAATTAGGAAGCTGTCAAGTTATGATCCT 60  
 Db 25 ACATATGTCGCGCTGCCATAGTGGACTAATTAGGAAGCTGTCAAGTTATGATCCT 84  
 Qy 61 CAAGAAGGATGAAAGAATGTTAGCTTAAMACATCTGGTAGATGATAC 120  
 Db 85 CAAGAAGGATGAAAGAATGTTAGCTTAAMACATCTGGTAGATGATAC 144

Qy 121 ATCAGTTTCATAGGAGATTGAGCATACTCAAATCGGAAAGTCACATGGAAGAACATCTGGTAGATGATAC 180  
 Db 145 ATCAGTTTCATAGGAGATTGAGCATACTCAAATCGGAAAGTCACATGGAAGAACATCTGGTAGATGATAC 204

Qy 181 GAATTTGTTGACTGGGACCAAAATSCACAGTGATCTGTGGATCTTG 240  
 Db 205 GAATTTGTTGACTGGGACCAAAATSCACAGTGATCTGTGGATCTTG 264

Qy 241 ATCCAAATGATTGCTCTGGAGCTTGTGGTCCAGATGCTGTCC 294  
 Db 265 ATCCAAATGATTGCTCTGGAGCTTGTGGTCCAGATGCTGTCC 318

RESULT 15  
 BC013316  
 LOCUS BC013316  
 DEFINITION Homo sapiens interleukin-1 receptor-associated kinase 4, mRNA (cDNA clone MGC:13330 IMAGE:287014), complete cds.  
 ACCESSION BC013316  
 VERSION BC013316.1  
 KEYWORD GT:15426431  
 SOURCE MGC  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1629)  
 AUTHORS Straubhaar, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schneider, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Cabavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiraku, S., Criminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Adelman, R.D., Mulahy, S.J., Bosak, S.H., Mcowan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., McRae, P.J., Richards, S., Wolley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shnechenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grinblat, J., Schmitz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalius, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBLMED 1247792

REFERENCE 2 (bases 1 to 1629)

AUTHORS Straubhaar, R.

TITLE Direct Submission

JOURNAL Submitted (31-AUG-2001) National Institutes of Health - Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NTH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Email: cgabes-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbiology.org>

contact: amadar@systemsbiology.org

Anup Madan, Jessie Farney, Brin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez, and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at: <http://image.l1nl.gov>

Series: IRAL plate 19 Row: n Column: 2<sup>4</sup>

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 705840.

Location/Qualifiers 1. 1629

FEATURES

SOURCE

gene

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 /db\_xref="LocusID:1135"  
 /db\_xref="GeneID:51135"  
 /db\_xref="MMR:606883"  
 /product="interleukin-1 receptor-associated kinase 4"  
 /protein\_id="AAH13316.1"  
 /db\_xref="GI:15426432"  
 /db\_xref="LocusID:51135"

ORIGIN

Query Match 99.5%; Score 292.4; DB 9; Length 1629;

Best Local Similarity 99.7%; Pred. No. 4.3e-64; Mismatches 0; Indels 0; Gaps 0;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACATATGTCGCGCTGCCATAGTGGACTAATTAGGAAGCTGTCAAGTTATGATCCT 60  
 Db 95 ACATATGTCGCGCTGCCATAGTGGACTAATTAGGAAGCTGTCAAGTTATGATCCT 154  
 Qy 61 CAAGAAGGATGAAAGAATGTTAGCTTAAMACATCTGGTAGATGATAC 120  
 Db 155 CAAGAAGGATGAAAGAATGTTAGCTTAAMACATCTGGTAGATGATAC 214

Qy 121 ATCAGTTTCATAGGAGATTGAGCATACTCAAATCGGAAAGTCACATGGAAGAACATCTGGTAGATGATAC 180  
 Db 215 ATCAGTTTCATAGGAGATTGAGCATACTCAAATCGGAAAGTCACATGGAAGAACATCTGGTAGATGATAC 274

Qy 181 GAATTTGTTGACTGGGACCAAAATSCACAGTGATCTGTGGATCTTG 240  
 Db 275 GAATTTGTTGACTGGGACCAAAATSCACAGTGATCTGTGGATCTTG 334

Qy 241 ATCCAAATGATTGCTCTGGAGCTTGTGGATCTTG 294  
 Db 335 ATCCAAATGATTGCTCTGGAGCTTGTGGATCTTG 388

Thu Jan 13 09:24:11 2005

us-10-001-254-5.rge

Page 9

Job time : 1848 sec8

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GenCore version 5.1.6  
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## Om protein - protein search, using sw model

Run on: January 10, 2005, 23:07:39 ; Search time 152 Seconds

231.286 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517

Sequence: I TYVRCVLNGLIRKLSDLFIDP.....LLIQNEFFPAPASLLLPDAVP 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04;\*

1: geneseq\_1980s;\*

2: geneseq\_1990s;\*

3: geneseq\_2000s;\*

4: geneseq\_2001s;\*

5: geneseq\_2002s;\*

6: geneseq\_2003s;\*

7: geneseq\_2003bs;\*

8: geneseq\_2004s;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	517	100.0	98	AAB24854
2	517	100.0	98	AAB38957
3	517	100.0	206	AAY2347
4	517	100.0	455	AEG12118
5	517	100.0	460	AAB24859
6	517	100.0	460	AAB24865
7	517	100.0	460	AAB24868
8	517	100.0	460	AAB38908
9	517	100.0	460	AAB389102
10	517	100.0	460	ABR4401
11	513	99.2	191	AAD04002
12	513	99.2	460	AAB05398
13	513	99.2	460	AAB05401
14	511	98.8	460	AAB05403
15	507	98.1	460	AAB05404
16	475	92.1	459	AAB05399
17	473	91.5	459	AAB05405
18	453	91.5	459	AAB05406
19	255	49.5	102	ABG12616
20	247	47.8	59	AAB24864
21	247	47.8	59	AAB28907
22	247	47.8	60	ABD28317
23	245	47.4	127	ABG12615
24	96.5	18.7	596	AAY29406
25	96.5	18.7	4	AAB65667

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

RESULT 1

AAB24854

AAB24854 Standard; peptide; 98 AA.

XX

AAB24854;

XX

22-OCT-2002 (first entry)

DT

Human IRAK4 DD. (death domain) protein.

XX

Human; death domain; DD; death effector domain; DED; Chlamydia infection;

NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; spsis;

inflammation; allergy; autoimmunity; allograft rejection; cell division;

immune-based pathology; fibrosis; arthritis; graft versus host disease;

immunosuppressive; gene therapy; antisense therapy.

XX

Human; death domain; DD; death effector domain; DED; Chlamydia infection;

NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; spsis;

inflammation; allergy; autoimmunity; allograft rejection; cell division;

immune-based pathology; fibrosis; arthritis; graft versus host disease;

immunosuppressive; gene therapy; antisense therapy.

OS

Homo sapiens.

XX

WO200240680-A2.

PN

XX

PD

23-MAY-2002.

XX

PP

15-NOV-2001; 2001W0-US044844.

XX

PR

17-NOV-2000; 2000US-0071593.

PR

29-JUN-2001; 2001US-0301889P.

XX

(BURN-) BURNHAM INST.

XX

Reed JC, Godzik A, Pawlowski K, Florentino L, Lee SH, Roth W,

PI

Stemmer-Liwen F;

XX

DR

WPI; 2002-500222/53.

DR

N-PSDB; RAD40074.

XX

New polypeptide comprising a death domain or death effector domain,

useful for discovery of drugs that suppress infection, inflammation,

allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX

Claim 1; Page 174; 209pp; English.

XX

The invention relates to an isolated polypeptide comprising a death

domain (DD), death effector domain (DED) or NB-ARC domain. The invention

is useful for identifying a binding agent, preferably a protein or a drug

that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC

domain from DR3, IRAK4, CRD (Chlamydia trachomatis DD protein), DED4 or

NIDD (NGFR-interacting Death Domain), with a candidate binding agent, or

detecting the association of the domain and the candidate binding agent,

CC

Aab248173 Interleuk

Aab2275 Human MAR

Aab48172 Interleuk

Aam38644 Human pol

Abg22715 Novel hum

Adb61346 Murine IR

Abg303007 Novel hum

Aay08653 Human IRA

Add40441 Human IRA

Aav08654 Human IRA

Aae37948 Murine My

Aab97836 Human cys

Aab41026 Human ORP

Abg61489 Human NP-

Aav97838 Human cys

Add04325 Antipsori

Adg92021 Human muc

Abg6115 Drosophil

Adk16042 Streptomy

Adf30722 Rat angio

by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTPD DD of *C. trachomatis*, *C. muridarum*, *C. pneumoniae*, and *C. psittaci* or a nucleic acid encoding the CTPD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD protein

by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the stress levels of a cell process such as cell proliferation, cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CmB DB or C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CmB DB protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for

discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD protein

	Query	Match	Similarity	Score	DB	Length
1	TIVRCVLNGLIRKLSDRIDPQBGWKKLAVALAKRPGSPDRYNOHIFRREALLQTGKSIS	100.0%	100.0%	517	5	98
1	TIVRCVLNGLIRKLSDIDPQEGWKKLAVALAKRPGSPGDNYNQHIFRREALLQTGKSIS	100.0%	100.0%	517	5	98
61	ELLFDKGITTCNTVGLDVLILLIQEPPASLLIPDAV	98	98	50	5	98
61	ELLFDKGITTCNTVGLDVLILLIQEPPASLLIPDAV	98	98	50	5	98

T 2  
T 987  
AAE38897 standard; protein: 98 AA.

18-DEC-2003 (first entry)  
Human IRAK4 DD protein.  
Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis; death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasoconstrictor; microbial infection; inflammation; allograft rejection; CDDD; cell stress response; benign prostatic Hyperplasia; antibacterial; NMD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IL-1R; IL-1R-associated kinase.

Homo sapiens.

PR 05-OCT-1998; 98US-00166350.  
 XX  
 PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX  
 PI Obata Y, Gout I, Tureci O, Sahin U, Pfreundschuh M, Scanlan MJ;  
 XX Jager E, Old LJ, Knauth A;  
 DR WPI; 2000-303774/26.  
 XX N-PSDB; AAA03319.  
 PT Preventing, diagnosing and/or treating disorders associated with abnormal  
 PT expression of human cancer associated antigens.  
 XX  
 PS Example 1; Page 92-93; 121pp; English.  
 XX  
 CC AAV92338-47 are encoded by novel genes isolated by SEREX screening from a  
 CC retail cancer cell line 1973104. They are cancer associated antigens  
 CC precursors. These gene products are useful in methods for preventing,  
 CC diagnosing and/or treating disorders, especially cancer, associated with  
 CC abnormal expression of human cancer associated antigens. The method  
 CC comprises contacting a sample from a subject with an agent that  
 CC specifically binds to the nucleic acid molecule or expression product (or  
 CC fragment) complexed with a human leukocyte antigen (HLA) molecule and  
 CC determining the interaction between the agent and the nucleic acid  
 CC molecule or the expression product as a determination of the disorder  
 XX  
 SQ Sequence 206 AA;

Query Match 100.0%; Score 517; DB 3; Length 206;  
 Best local Similarity 100.0%; Pred. No. 5.2e-60;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TYVRCLNVGJRKLSDFPQEGWKLAVAIKKRSGDDRYNQFHIRRFEALLQTKSPS 60  
 Db 9 TYVRCLNVGJRKLSDFPQEGWKLAVAIKKRSGDDRYNQFHIRRFEALLQTKSPS 68  
 Qy 61 BLFDPWGTTCTVGLDVLDLQNEFPAPASLLPDAVP 98  
 Db 69 BLFDPWGTTCTVGLDVLDLQNEFPAPASLLPDAVP 106  
 RESULT 4  
 ABC12618  
 ID ABC12618 standard; protein; 455 AA.  
 XX  
 AC ABC12618;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #12609.  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 XX WO2001175067-A2.  
 PD 11-OCT-2001.  
 XX  
 PP 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 XX 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR N-PSDB; AAS76805.  
 XX  
 New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 42977; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABC0010-ABC3377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC [ftpt.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
 XX  
 SQ Sequence 455 AA;

Query Match 100.0%; Score 517; DB 4; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-59;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVRCLNVGJRKLSDFPQEGWKLAVAIKKRSGDDRYNQFHIRRFEALLQTKSPS 60  
 Db 9 TYVRCLNVGJRKLSDFPQEGWKLAVAIKKRSGDDRYNQFHIRRFEALLQTKSPS 68  
 Qy 61 BLFDPWGTTCTVGLDVLDLQNEFPAPASLLPDAVP 98  
 Db 69 BLFDPWGTTCTVGLDVLDLQNEFPAPASLLPDAVP 106

RESULT 5  
 AAE24859  
 ID AAE24859 standard; protein; 460 AA.  
 XX  
 AC AAE24859;  
 XX  
 DE 22-OCT-2002 (first entry)  
 XX  
 DB Human IRAK4 protein #1.  
 XX  
 Human; death domain; DD: death effector domain; DED: Chlamydia infection;  
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KW immune-based pathology; arthritis; graft versus host disease;  
 KW immunosuppressive; gene therapy; antisense therapy.  
 XX  
 Homo sapiens.  
 XX  
 WO200240680-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PP 15-NOV-2001; 2001WO-US044844.  
 XX  
 PR 17-NOV-2000; 2000US-00715893.  
 PR 29-JUN-2001; 2001US-0301889P.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Godzik A, Pawlowski K, Florentino L, Lee SH, Roth W;

PI	Steinmer-Liween, F.	XX	PD	23-MAY-2002.
DR	WPI; 2002-500222/53.	XX	PP	15-NOV-2001; 2001WO-US044844.
DR	N-PSDB; AAD40079.	XX	PR	17-NOV-2000; 2000US-0071593.
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.	XX	PR	29-JUN-2001; 2001US-0301889P.
PS	Claim 3; Page 183-184; 209pp; English.	XX	PA	(BURN-) BURNHAM INST.
CC	The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from IRAK3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DEBD4 or NTDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for detecting bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 protein	CC	PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W; Steinmer-Liween, F.
CC	Sequence 460 AA;	XX	PI	Steinmer-Liween, F., Pawlowski K, Fiorentino L, Lee SH, Roth W; Steinmer-Liween, F.
Query Match	100.0%; Score 517; DB 5; Length 460;	XX	PS	Claim 1; Page 196-197; 209pp; English.
Best Local Similarity	100.0%; Pred. No. 1.6e-59;	XX	CC	The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAPS, IRAK4, CTDD (Chlamydia trachomatis DD protein), DEBD4 or NTDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for detecting bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 protein
Matches	98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	CC	Sequence 460 AA;
Qy	1 TVYRCVLNGLIRKLSDFTDPOEGWKVLAVKIKPSPGDDRYNOFHIRFEALLOQTGSKPTS 60	Db	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
Qy	9 TYVRCLANGLIRKLSDFTDPOEGWKVLAVKIKPSPGDDRYNOFHIRFEALLOQTGSKPTS 68	Db	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
Db	61 ELLFDWGTTCTVGLDVLLIONEFPAPASLLIDAVP 98	Db	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	69 ELLFDWGTTCTVGLDVLLIONEFPAPASLLIDAVP 106	Db	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
RESULT 6		Db	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
ID	AAE24865	Db	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	AAE24865 standard; protein; 460 AA.	Db	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
AC	AAE24865;	Db	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
XX	22-OCT-2002 (first entry)	Db	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE	Human IRAK4 protein #2.	Db	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
XX		Db	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
KW	Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immuno-suppressive; gene therapy; antisense therapy.	XX	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Homo sapiens.	XX	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
XX		XX	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
PN	WO200240680-A2.	XX	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		XX	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
RESULT 7		XX	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
AAE38908		XX	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	AAE38908 standard; protein; 460 AA.	XX	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
XX		XX	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;
AC	AAE38908;	XX	CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	18-DEC-2003 (first entry)	XX	CC	Query Match 100.0%; Score 517; DB 5; Length 460;
DE	Human IRAK4 protein #2.	XX	CC	Best Local Similarity 100.0%; Pred. No. 1.6e-59;

KW Human; death Domain; DD; death effector domain; DED; cell proliferation; KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; KW neural growth factor receptor-interacting death domain; cell adhesion; KW vasoconstrictor; microbial infection; inflammation; allograft rejection; CTDD; KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK.

XX Homo sapiens.

OS Homo sapiens.

XX US2003049702-A1.

XX PD 13-MAR-2003.

XX PP 15-NOV-2001; 2001US-00001254.

XX PR 17-NOV-2000; 2000US-00715893.

PR 17-NOV-2000; 2000US-0367360P.

PR 29-JUN-2001; 2001US-0301889P.

XX (REED/) REED J C.

PA (GODZ/) GODZIK A.

PA (PAWL/) PAWLOWSKI K.

PA (FLOR/) FIORENTINO L.

PA (LEBS/) LEE S H.

PA (ROTH/) ROTH W.

PA (STEN/) STENNER-LIEWEN F.

XX PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PT Steiner-Liewen F;

XX DR WPI; 2002-500222/53.

DR N-ISDB; Aad59067.

XX PT New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX PS Claim 1; Page 53-54; 99pp; English.

XX CC The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC domains and/or anti-DD anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases.

CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human

CC Sequence 460 AA;

XX Query Match 100.0%; Score 517; DB 5; Length 460;

Best Local Similarity 100.0%; Pred. No. 1.6e-59;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYVRCLNVGLIRKSLDPDQEGKKLAVAKKPKSGDPRYQHRRREALQGKSPTS 60

Db 9 TYVRCLNVGLIRKSLDPDQEGKKLAVAKKPKSGDPRYQHRRREALQGKSPTS 68

QY 61 ELLFDWGTTCTGDLVLDLQINERFPAASILLDAVP 98

Db 69 ELLFDWGTTCTGDLVLDLQINERFPAASILLDAVP 106

RESULT 8

AAE38902 standard; protein; 460 AA.

XX AAE38902:

XX AC AAE38902:

XX DT 18-DEC-2003 (first entry)

XX DE Human IRAK4 protein #1.

XX PR Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasoconstrictor; microbial infection; inflammation; allograft rejection; CTDD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domains 9..106 /note= "Death domain of IRAK-4"

XX PN US2003049702-A1.

XX PR 13-MAR-2003.

XX PR 15-NOV-2001; 2001US-00001254.

XX PR 17-NOV-2000; 2000US-00715893.

PR 17-NOV-2000; 2000US-0367360P.

PR 29-JUN-2001; 2001US-0301889P.

XX PA (REED/) REED J C.

PA (GODZ/) GODZIK A.

PA (PAWL/) PAWLOWSKI K.

PA (FLOR/) FIORENTINO L.

PA (LEBS/) LEE S H.

PA (ROTH/) ROTH W.

PA (STEN/) STENNER-LIEWEN F.

XX PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PT Steiner-Liewen F;

XX DR WPI; 2002-500222/53.

N-ISDB; Aad59061.

XX PT New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX PS Claim 2; Fig 10B; 99pp; English.

XX The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion,

cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DBs, DBs and NB-ARC domains and/or anti-DD, anti-DB or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte, hyperplasia, neoplasia, Keloid, benign prostatic hyper trophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 protein.

Sequence 460 AA;

Query Match	100.0%	Score	517	DB	5	Length	460
Best local Similarity	100.0%	Pred.	No.	1.6e-59			
Matches	98	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

QY 1 TYVRCLANGLIRKUSDPIDPQEGWKLAVAIKKPSGDDRINQPHIRRFEALLQTGSPTS 60  
Db 9 TYVRCLANGLIRKUSDPIDPQEGWKLAVAIKKPSGDDRINQPHIRRFEALLQTGSPTS 68

QY 61 ELLFDWGTTCTVGLDVLILLIQNEFPAPASLLPDAVP 98  
Db 69 ELLFDWGTTCTVGLDVLILLIQNEFPAPASLLPDAVP 106

RESULT 9

ID	ABR44401	Standard; protein; 460 AA.
XX		
AC	ABR44401;	
XX		
DT	11-JUL-2003 (first entry)	
DE	Human IL-1 receptor-associated kinase-4 amino acid sequence.	
XX		
KW	Antisense; therapy; cyrostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003028636-A2.	
XX		
PD	10-APR-2003.	
XX		
PP	26-SEP-2002; 2002WO-US030574.	
XX		
PR	28-SEP-2001; 2001US-00966451.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett FC, Freier SM;	
XX		
DR	WPI; 2003-363256/34.	
XX		
DR	N-FSDB; ACC47548.	
XX		
PT	New antisense oligonucleotides for modulating IL-1 receptor-associated kinase-4 gene expression, particularly useful for preventing, delaying or treating e.g. cancer (e.g. renal cancer), inflammatory disease or an infection.	
XX		
PS	Example 13; Page 80-83; 119pp; English.	
XX		
CC	The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridizing with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridizing with an 8-nucleotide portion of an active site on a nucleic acid molecule encoding IL-1 receptor associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or	

cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DBs, DBs and NB-ARC domains and/or anti-DD, anti-DB or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte, hyperplasia, neoplasia, Keloid, benign prostatic hyper trophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation following balloon angioplasty (restenosis). The present sequence is human interleukin-1 receptor-associated kinase-4 protein.

Sequence 460 AA;

Query Match	100.0%	Score	517	DB	6	Length	460
Best local Similarity	100.0%	Pred.	No.	1.6e-59			
Matches	98	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

QY 1 TYVRCLANGLIRKUSDPIDPQEGWKLAVAIKKPSGDDRINQPHIRRFEALLQTGSPTS 60  
Db 9 TYVRCLANGLIRKUSDPIDPQEGWKLAVAIKKPSGDDRINQPHIRRFEALLQTGSPTS 68

QY 61 ELLFDWGTTCTVGLDVLILLIQNEFPAPASLLPDAVP 98  
Db 69 ELLFDWGTTCTVGLDVLILLIQNEFPAPASLLPDAVP 106

RESULT 10

ID	ADO44001	Standard; protein; 460 AA.
XX		
AC	ADO44001;	
XX		
DT	15-JUL-2004 (first entry)	
DE	Amino acid sequence of human IRAK4.	
XX		
KW	protein complex; neurological disease; stroke; neurodegeneration; Wallerian degeneration; Alzheimer's disease; neurological disorder; epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease; atherosclerosis; imid-MYO-inositol triphosphate 3 kinase A; ASK1; ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha; Cdc37; CHK2; CTCL tumour antigen SE20-4; ER-1 alpha 1; ENAP; FLJ14553; NTR2RP202252; FLJ30039; FEBR2020249; HRC2; inositol polyphosphatase-5-phosphatase; inositol-1,4,5-triphosphate-5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MST030; Nek9; PAR3; Peillin 1; Peillin 3; podocalyxin-like protein 1 precursor; Pushover; S-adenosylhomocysteine; secretory carrier-associated membrane protein 2; surfactin locus protein 2; ubiquitin carboxyl terminal hydrolase 11; upstream regulatory element binding protein 1; Varkul; Werner's syndrome helicase interacting protein; WHIP; X-ray repair cross complementing protein 4.	
XX		
KW	X-ray repair cross complementing protein 4.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004031242-A2.	
XX		
PD	15-APR-2004.	
XX		
PP	11-SEP-2003; 2003WO-EP010110.	
XX		
PR	12-SEP-2002; 2002EP-00020435.	
PR	12-SEP-2002; 2002EP-00020436.	
PR	12-SEP-2002; 2002EP-00020497.	
XX		
PA	(CELL-) CELLZONE AG.	
XX		
PI	Bouwmeester T, Drewes G, Jackson D, Helftnebein G, Schirle M;	
PI	Kuester B, Hopf C;	
XX		
DR	WPI; 2004-316467/29.	

conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The antisense compounds are useful for diagnostics, therapeutics, prophylaxis, or as research reagents or kits. The current sequence represents the human IL-1 receptor-associated kinase-4 amino acid sequence.

Sequence 460 AA;

Query Match	100.0%	Score	517	DB	6	Length	460
Best local Similarity	100.0%	Pred.	No.	1.6e-59			
Matches	98	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

QY 1 TYVRCLANGLIRKUSDPIDPQEGWKLAVAIKKPSGDDRINQPHIRRFEALLQTGSPTS 60  
Db 9 TYVRCLANGLIRKUSDPIDPQEGWKLAVAIKKPSGDDRINQPHIRRFEALLQTGSPTS 68

New complex comprising at least one first protein, and at least one second protein, useful for treating stroke, Alzheimer's disease, neurological disorders such as epilepsy, and inflammatory conditions such as ulcerative colitis.

PS Example; Page 213-214; 287pp; English.

XX CC The specification describes protein complexes involved in cellular processes which have been shown to be critical for the development of various forms of neurological diseases. Three protein complexes were identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3 protein complex. The protein complex are useful for treating diseases and disorders, e.g., stroke, neurodegeneration such as Wallerian degeneration, Alzheimer's disease, neurological disorders such as epilepsy, and inflammatory conditions such as ulcerative colitis, Crohn's disease or atherosclerosis. Proteins identified as being part of the protein complexes of the invention are 1D-MYO-inositol triphosphate 3 kinase A, ASKL, ASK2, ASK3, CAMKII delta, CamkII gamma, casein kinase II alpha, Cdc27, CRK2, CTCL tumour antigen SB20-4, EF-1 alpha 1, EMP, PLX14653 NT2R2002259, PLJ30339 FR2A020429, HERC2, two hypothetical proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase, inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA441, MSTN030, Nek9, PAR6, Pellino 3, podocalyxin-like protein 1 precursor, Pushover, a putative S-adenosylhomocysteinase, secretory carrier-associated membrane protein 2, Surfeit locus protein 2, ubiquitin carboxyl terminal hydrolase 11, upstream regulatory element binding protein 1, Vartul, Werner' syndrome helicase interacting protein (WRIP), X-ray repair cross complementing protein 4 (isoform 1). The present sequence represents IRAK4.

XX CC Sequence 460 AA;

XX SQ Query Match 100.0%; Score 517; DB 8; Length 460; Best Local Similarity 100.0%; Pred. No. 1.6e-59; Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYVRCLANGLIRKLSDFPQEGWKKLAVAIKKPGSDDRYNQFHIRFEALLQTKSPS 60  
9 TYVRCLANGLIRKLSDFPQEGWKKLAVAIKKPGSDDRYNQFHIRFEALLQTKSPS 68

Db 61 ELLFDWGTTCTVGDIVDILIONERFPASILLPDAVP 98  
69 ELLFDWGTTCTVGDIVDILIONERFPASILLPDAVP 106

RESULT 11

ID AAE05402 standard; protein; 191 AA.

AC AAE05402;

XX DT 24-SEP-2001 (first entry)

XX DR Truncated form of human IRAK-4 protein.

XX KW Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; IL; antibacterial; antiinflammatory; ophthalmological; vagotrop; opp; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; sarcoidosis; transgenic animal; mutant; mutain.

OS Homo sapiens.

OS Synthetic.

XX PN WO20151641-A1.

XX PD 19-JUL-2001.

XX PP 12-JAN-2001; 2001WO-US001171.

PR XX 13-JAN-2000; 2000US-0176395P.

---

XX PA (TULSA-) TULARIK INC.

XX PR Wesche H, Li S;

XX DR WPI; 2001-451860/48.

XX PT Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

XX RS Claim 53; Page: 89pp; English.

XX The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK) -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)- $\kappa$ B activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, barcodiosis and ophthalmic diseases and conditions. The inhibitors of IRAK-4 activity or expression are used to inhibit signal transduction resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NF $\kappa$ BA in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy. The present sequence is the truncated form of human IRAK-4 protein. This sequence was constructed by deleting the residues after K191 in the wild type human IRAK-4 protein. This truncated form is the dominant negative form of human IRAK-4 protein. Note: This sequence is not shown in the specification but is derived from human IRAK-4 (SEQ ID NO: 1) shown in figure 1 of the specification (AAE05398).

XX SQ Sequence 191 AA;

XX Query Match 99.2%; Score 513; DB 4; Length 191; Best Local Similarity 99.0%; Pred. No. 1.6e-59; Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVRCLANGLIRKLSDFPQEGWKKLAVAIKKPGSDDRYNQFHIRFEALLQTKSPS 60  
9 TYVRCLANGLIRKLSDFPQEGWKKLAVAIKKPGSDDRYNQFHIRFEALLQTKSPS 68

Db 61 ELLFDWGTTCTVGDIVDILIONERFPASILLPDAVP 98  
69 ELLFDWGTTCTVGDIVDILIONERFPASILLPDAVP 106

RESULT 12

ID AAE05398 standard; protein; 460 AA.

ID AAE05398

AC AAE05398;

XX DT 24-SEP-2001 (first entry)

XX DB Human interleukin-1 (II-1) receptor-associated kinase (IRAK)-4 protein.

Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosstatic; IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumor; Lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 5..147 /label= Death domain

FT /note= "Also known as N-terminal domain"

FT 192..460 /label= Central\_kinase\_domain

FT Domain

PN WO200151641-A1.

XX

PD 19-JUL-2001.

XX

PR 12-JAN-2001; 2001WO-US001171.

XX

PR 13-JAN-2000; 2000US-0176395P.

PA (TULA-) TULARIK INC.

XX

PT Wesche H, Li S;

PT WPI; 2001-451860/48.

DR N-PSDB; AAD10197.

XX

PT Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

PS Claim 17; Fig 1; 89pp; English.

XX

The present sequence is human interleukin (IL)-1 receptor associated kinase (IRAK)-4 protein. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, psoriasis, disease of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, sarcoidosis and ophthalmic diseases and conditions. The inhibitors of IRAK-4 activity or expression are used to inhibit signal transduction resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NF-kappaB in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy

XX Sequence 460 AA;

XX

Query Match 99.2%; Score 513; DB 4; Length 460; Best Local Similarity 99.0%; Pred. No. 5..3e-59;保守性 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TYRGLDNVNLIRKSDFDPQSEGKKAVALRKPSDDDRNQPHRRFEALIQGKSPS 60

Db 9 TYRCLNVLGILRLSDFDPQSEGKKAVALRKPSDDDRNQFHIRRFEALIQGKSPS 68

Qy 61 ELIFDWGTRNTCTWGDLLDILLIONEFPFRPASILLPDPWP 98

Db 69 ELLFDWGSTINCTWGDLLDILLIONEFPFRPASILLPDPWP 106

RESULT 13

ID AAE05401 standard; protein; 460 AA.

ID AAE05401

AC AAE05401;

XX DT 24-SEP-2001 (first entry)

XX DE Human IRAK-4 mutant (K213A, K214A).

XX Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosstatic; IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumor; Lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal; mutant; mutein.

XX OS Homo sapiens.

XX OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 213

FT /note= "Wild type Lys substituted with Ala"

FT /note= "Wild type Lys substituted with Ala"

XX

PN WO200151641-A1.

XX

PD 19-JUL-2001.

XX

PR 12-JAN-2001; 2001WO-US001171.

XX

PR 13-JAN-2000; 2000US-0176395P.

PA (TULA-) TULARIK INC.

XX

PT Wesche H, Li S;

PT WPI; 2001-451860/48.

XX

PT Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

PS Claim 51; Page: 89pp; English.

XX

The patient discloses interleukin (IL)-1 receptor associated kinase (IRAK) -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory



XX  
 KW Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic;  
 KW IL; antibacterial; antiinflammatory; ophthalmological; vasoconstrictive; OBD;  
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;  
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;  
 KW interstitial lung disease; allergic rhinitis; transplant rejection;  
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;  
 KW multiple sclerosis; diabetes; cancer; solid tumor; lymphoma; stroke;  
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;  
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;  
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;  
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/toll receptor;  
 KW sarcoidosis; transgenic animal; mutant; mutein; variant; polymorphism;  
 XX OS Homo sapiens.  
 OS Synthetic.

SQ Sequence 460 AA:  
 Query Match 98.1%; Score 507; DB 4; Length 460;  
 Best Local Similarity 98.0%; Pred. No. 3. 4e-58; 2; Indels 0; Gaps 0;  
 Matches 96; Conservative 0; Mismatches 2; Gaps 0;  
 QY 1 TYVRCLNVLIRKLSDFDPOGCKLAVAIKPKSGDDRNYQHRRFEALQGKSPS 60  
 Db 9 TYVRCLNVLIRKLSDFDPOGCKLAVAIKPKSGDDRNYQHRRFEALQGKSPS 68  
 KW 61 ELLFDWGTTNCWGDVLDLILQNEFPRAPASLLPDPW 98  
 QY 69 ELLFDWGTTNCWGDVLDLILQNEFPRAPASLLPDPW 106  
 Db

Search completed: January 10, 2005, 23:21:49  
 Job time : 155 secs

Key Location/Qualifiers  
 Misc-difference 17 /note= "Wild type GLY substituted with Ala"

WO200151641-A1.

PN 19-JUL-2001.

PP 12-JAN-2001; 2001WO-US001171.

PR 13-JAN-2000; 2000US-0176395P.

XX PA (TULLA-) TULARIK INC.

XX PI Wesche H, Li S;

XX DR WPI; 2001-451860/48.

XX Disclosure; Page: 8pp; English.

Novel human interleukin-1 receptor associated kinase polypeptide, useful  
 PT for identifying modulators of the polypeptide for treating gout, asthma,  
 PT allergic rhinitis, multiple sclerosis and skin cancer.

XX Disclosure; Page: 8pp; English.

The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)  
 CC -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-1<sub>B</sub>  
 CC and other receptors and act to transduce signals originating from the  
 CC activated receptors, ultimately leading to a variety of downstream  
 CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4  
 CC inhibitors are useful for treating inflammatory diseases such as  
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory  
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD),  
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or  
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,  
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or  
 CC diabetes), cancer (e.g., solid tumors, skin cancer or lymphoma),  
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of  
 CC the central nervous system (e.g., neurodegenerative disease), CD14  
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,  
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic  
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and  
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,  
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of  
 CC IRAK-4 activity or expression are used to inhibit signal transduction  
 CC resulting from the activation of an interleukin-1 receptor (IL-1R)/toll  
 CC receptor in a cell. They also inhibit the activation of a transcription  
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a  
 CC nonhuman transgenic animal which is useful for testing the function of  
 CC IRAK-4 in vivo. To generate models for the study of inflammatory  
 CC disorders and conditions and for the development of potential treatments  
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences  
 CC are also used in gene therapy and in antisense therapy. The present  
 CC sequence is a polymorphic variant (G17A) of human IRAK-4 protein. Note:  
 CC this sequence is not shown in the specification but is derived from human  
 CC IRAK-4 (SEQ ID NO: 1) shown in figure 1 of the specification (AAE05398).  
 XX



Proc. Natl. Acad. Sci. U.S.A. 88, 810-814, 1991  
 A;Title: Genetic and molecular characterization of tube, a *Drosophila* gene maternally re  
 A;Reference number: A37862; MUID:9126085; PMID:1899484  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-162 <BET>  
 A;Cross-references: UNIPROT:P22812; GB:MS9501; NID:9158750; PID:9158751  
 C;Genetics:  
 A;Gene: FlyBase:tub  
 A;Cross-family: Drosophila tube protein  
 C;Superfamily:  
 Query Match 13.9%; Score 72; DB 2; Length 462;  
 Best Local Similarity 24.8%; Pred. No. 4;  
 Matches 28; Conservative 16; Mismatches 39; Indels 30; Gaps 4;  
 Qy 11 IRKLSFIDPOEGWKKLAVAIKKPSGDD-----RY--NQFHIRR 47  
 Db 41 IYRLAKTILDENSCWRKLMSII--PKGMVQACSGAGCLNPALIKKGKFTAQDFQIDE 98  
 Qy 48 FEALIQTGKPTSELLFDW3IT----NCWYGDLYDILLNEFFPASLLPD 95  
 Db 99 AANRUPPDQSKSQQMIDEWKTSKGLNERPFTVGVLQLVAPBLISAAFDVAFD 151

RESULT 3

A24700 apolipoprotein A-I precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004  
 C;Accession: A24700; S00298; A0514  
 R;Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.  
 J. Biol. Chem. 261, 13268-13277, 1986  
 A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-  
 A;Reference number: A92558; MUID:87008540; PMID:3020028  
 A;Accession: A24700  
 A;Molecule type: DNA  
 A;Residues: 1-259 <HAD>  
 A;Cross-references: UNIPROT:P04639; EMBL:J02597; NID:9202935; PIDN:AAA40745.1; PID:92029  
 R;Poncin, J.R.; Martial, J.A.; Gielien, J.E.  
 Eur. J. Biochem. 140, 493-498, 1984  
 A;Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.  
 A;Reference number: S00298; MUID:84207987; PMID:6426956  
 A;Accession: S00298  
 A;Molecule type: mRNA  
 A;Residues: 1-259 <PON>  
 A;Cross-references: GB:MM00001; EMBL:X00558; NID:9202944; PIDN:AAA40749.1; PID:9202945  
 R;Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.  
 J. Biol. Chem. 257, 971-978, 1982  
 A;Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an  
 A;Reference number: A05314; MUID:82098162; PMID:6798036  
 A;Accession: A05314  
 A;Molecule type: protein  
 A;Residues: 1-18, X, 20-21, X', 23-28, X', 30-38, X', 40-41, X', 43-45 <GOR>  
 C;Comment: This protein is synthesized in the liver and small intestine. The propeptide  
 C;Genetics: This protein is a major component of the high density lipoproteins in plasma.  
 A;Intron: 15/1; 66/2  
 C;Superfamily: apolipoprotein A-I  
 C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipc  
 F;1-18/Domain: signal sequence #status experimental <SG>  
 F;1-24/Domain: propeptide #status experimental <PRO>  
 F;25-259/Domain: apolipoprotein A-I #status experimental <MAT>  
 Query Match 13.7%; Score 71; DB 2; Length 259;  
 Best Local Similarity 31.2%; Pred. No. 2.5; Matches 24; Conservative 8; Mismatches 31; Indels 14; Gaps 3;

Qy 19 DPOEQEWKLLA-----VAIKEPKSGDQRDRYQPHIRREALIQTGKPTSELLFDW3ITNTCT 72  
 Db 26 EPQSOWDRVKDFAVVYDAVDSGRDVYSPFESSTL----GKQNLNLDNWDTLGST 79

RESULT 4

B64226 type I restriction enzyme M protein - Helicobacter pylori (strain 26695)  
 C;Species: Helicobacter pylori  
 C;Accession: B64226  
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalil, H.G.; Glodek, A.; McKeown, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Natur, 388, 539-547, 1997  
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.; A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A;Accession: B64226  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Residues: 1-527 <TOM>  
 A;Cross-references: UNIPROT:O25521; GB:AE000596; GB:AE000511; NID:92313982; PIDN:AAD0789  
 C;Superfamily: type I site-specific deoxyribonuclease chain fold  
 Query Match 13.1%; Score 67.5; DB 2; Length 527;  
 Best Local Similarity 31.1%; Pred. No. 15; Matches 19; Conservative 11; Mismatches 28; Indels 3; Gaps 1;  
 C;Accession: A10284  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.; Gao-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 433, 523-527, 2001  
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB0001; MUID:2147041; PMID:11586360  
 A;Accession: A10284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-334 <KUR>  
 A;Cross-references: UNIPROT:Q8Z248; GB:ALE90842; PIDN:GAC91141.1; PID:91598033; GSPDB:GI  
 A;Gene: YPO236

RESULT 5

A10284 probable exported protein YPO2336 [imported] - *Yersinia pestis* (strain C092)  
 C;Species: *Yersinia pestis*  
 C;Accession: A10284  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.; Gao-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 433, 523-527, 2001  
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB0001; MUID:2147041; PMID:11586360  
 A;Accession: A10284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-334 <KUR>  
 A;Cross-references: UNIPROT:Q8Z248; GB:ALE90842; PIDN:GAC91141.1; PID:91598033; GSPDB:GI  
 A;Gene: YPO236

Query Match 13.0%; Score 67; DB 2; Length 334;  
 Best Local Similarity 26.5%; Pred. No. 9.8; Matches 22; Conservative 11; Mismatches 24; Indels 26; Gaps 3;

Qy 16 DFIDPOEQEWKLLA-----VAIKEPKSGDQRDRYQPHIRREALIQTGKPTSELLFDW3ITNTCT 75  
 Db 209 DFLTMDEQWKKGIDGQHSTNSFSFLM--EKITDNKSRWS-----TTN---- 254

Qy 76 LVDLQIERRPASLLPD 98  
 Db 255 -----PMNYITADAPP 265

RESULT 6

C64714

translation elongation factor EF-Ts - *Helicobacter pylori* (strain 26695)  
 C;Species: *Helicobacter pylori*  
 C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
 C;Accession: C64714  
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Kharak, H.G.; Glodek, A.; McKenna  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
 Nature 368, 559-547, 1997  
 A;Authors: Walin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
 A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
 A;Reference number: A64520; MUID:97394467; PMID:9252185  
 A;Accession: C64714  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-355 <STO>  
 A;Cross-references: UNIPROT:P55975; GB:AE000653; GB:AE000511; NID:g2314733; PIDN:AAD0859  
 C;Superfamily: translation elongation factor EF-Ts

Query Match 13.0%; Score 67; DB 2; Length 355;  
 Best Local Similarity 22.9%; Pred. No. 11; Matches 24; Conservative 17; Mismatches 34; Indels 30; Gaps 3;  
 Matches 24; Conservative 17; Mismatches 34; Indels 30; Gaps 3;

QY 11 IRKLSDPFDPOBGWKKLAVAIKKPSGDDRNQFHI-----RREFAALONG--- 55  
 Db 78 INSEDTFVAKNEGKEL--VKKLTFTIKAHNHTFEELIKSPUNKPFFEEYLHSQIAVI 134  
 QY 56 -----KSPTESELFDWGTTNTCTVGDLVLILLIONEFFAP 88  
 Db 135 GENILVRKIAHLKAPSSHINGYAHNSNARVQVGLIGIKYDNEKNAP 179

RESULT 7

S76848 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)C;Species: *Synechocystis* sp.

A;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: S76848

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.  
 A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-299 <KAN>

A;Cross-references: UNIPROT:PT4644; EMBL:D99917; GB:AB001339; NID:gi1653836; PIDN:BA11876  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C;Genetics:  
 A;Start codon: GTG

Query Match 12.9%; Score 66.5; DB 2; Length 299;

Best Local Similarity 28.4%; Pred. No. 9.8; Matches 23; Conservative 16; Mismatches 37; Indels 5; Gaps 3;

QY 12 RKLSDPFDPOBGWKKLAVAIKKPSGDDRNQFHIIRFEALONG--- 70  
 Db 159 RKLADKLERGY-LGVYVYKPS--HFTYNNPSKOEKLEDISQYRHTIISYFSDE 214  
 QY 71 CTVGLDVLDLJLQNELLPASTI 91  
 Db 215 GTVNDLIDQFVNQAFADLAI 235

RESULT 8

B96333 hypothetical protein FB45\_28 [imported] - *Arabidopsis thaliana*C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: B96633

R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Dev. Biol. 192, 323-339, 1997

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Andersen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Wu, D.; Yu, G.; Fraser, C.M.; Venier, J.C.; Davis, R.W.; ker, M.; Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:1130712

A;Accession: B96633  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-491 <STO>  
 A;Cross-references: UNIPROT:022714; GB:AE0005173; NID:g2462744; PIDN:AAB71963.1; GSDB:GN-000066  
 C;Genetics:  
 A;Gene: F8A5.28  
 A;Map position: 1

Query Match 12.9%; Score 66.5; DB 2; Length 491;  
 Best Local Similarity 26.3%; Pred. No. 18; Matches 20; Conservative 15; Mismatches 34; Indels 7; Gaps 2;

QY 8 VGLIRKLSDFDPOBGWKKLAVAIKKPSGDDRNQFHIIRFEALONG--- 67  
 Db 271 ITLYGRKGKJTEVYRIRSLRAIPKTS----NVAYNMIQIVLVKLNDLPGASTLFKEW 325  
 QY 68 TTNCVGD--LVDLI 81  
 Db 326 QANCCTYDRLIVNL 341

RESULT 9

T50228 conserved hypothetical protein SPAC607.08c [imported] - fission yeast (*Schizosaccharomyces pombe*)C;Species: *Schizosaccharomyces pombe*

C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
 C;Accession: T50228

R;Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, December 1999

A;Reference number: Z25047

A;Accession: T50228

A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA

A;Residues: 1-579 &lt;ZIM&gt;

A;Cross-references: UNIPROT:OGUS10; EMBL:ALJ35751; PIDN:CAR63795.1; GSDB:GN00066; SPDB:

A;Experimental source: Strain 972n(-); cosmid c607

C;Genetics:

A;Gene: SPDB:SPAC607.08C

A;Map position: 1

C;Superfamily: *Caenorhabditis elegans* hypothetical protein F35B11.3

Query Match 12.9%; Score 66.5; DB 2; Length 579;

Best Local Similarity 30.8%; Pred. No. 22; Matches 28; Conservative 30; Mismatches 39; Indels 11; Gaps 5;

QY 6 LNVGLIRKUSDFDPOBGWKKLAVAIKKPSGDDRNQFHIIRFEALONG--- 64  
 Db 268 VTIGISGWLDGYNEVDAWKSLSITWGDKSTYWGDIYALKFEV--EALVBLGKS-LSRLP 323  
 QY 65 DWGTTNTCTVGDLVLILLQNEFFAP-ASLILP 94  
 Db 324 SAG----LGWVKGEBVISRTILAPLAALWP 349

RESULT 10

T30213 G-cadherin - sea urchin (*Lytechinus variegatus*)C;Species: *Lytechinus variegatus* (variegated urchin)

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T30213

R;Miller, J.R.; McClay, D.R.

Dev. Biol. 192, 323-339, 1997

A;Title: Characterization of the role of cadherin in regulating cell adhesion during set  
A;Reference\_number: 220780; Muid:98104238; PMID:9441671  
A;Accession: T3013  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2809 <ML>  
A;Cross-references: UNIPROT:O61230; EMBL:U34823; NID:g2982186; PID:g2982187; PID: AAC067

QY	26	KLAVALKKPSGGDDRYNQPHIRFEALIQTGKSPSTSLLFDWGTTCTVGDLVDLIIQER	12.9%; Score 66.5; Pred. No. 1. 5e+02; Length 2809;
QY	32	41; Best Local Similarity	32.4%; Pred. No. 1. 5e+02; Length 2809;
Db	173	RHIFIKAPIDMTTSQYHLEWVASDLDLSKA-TAELLIIVDATANQVPLVK-BSTNQF	Matches 24; Conservative 32; Mismatches 35; Indels 3; Gaps 3; QY 86 FAPAS-LILPDAVP 98
Db	173	RHIFIKAPIDMTTSQYHLEWVASDLDLSKA-TAELLIIVDATANQVPLVK-BSTNQF	85 230

RESULT 11  
882339 hypothetical protein XP0172 [imported] - *Xylella fastidiosa* (strain 9a5c)  
C;Species: *Xylella fastidiosa*  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;accession: 32666

Nature anonymous The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis; title: The genome sequence of the plant pathogen *Xylella fastidiosa*. Nature 406 151-157, 2000. A; reference number: A8215; MIMID:20365717; PMID:10910347 A; note: For a complete list of authors see reference number A59328 below A; status: preliminary A; molecule type: DNA A; species: *Xylella fastidiosa*.

**A.1. Authors:** Martínez, M.A.; Martínez, M.A.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E.; Matos, A.M.B.N.; Madeira, H.Y.H.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Oliveira, M.A.; Oliveira, M.C.; de Oliveira, M.C.; Palomari, D.P.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, M.; Tsuhako, M.H.; Vallada, H.; van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. **A.2. Reference number:** A29328 **A.3. Contents:** annotation

Query Match 12.8%; Score 66; DB 2; Length 598;  
 Best Local Similarity 31.0%; Pred. No. 26;  
 Matches 22; Conservative 8; Mismatches 31. Indels 10. Gaps 3.

RESULT 12

Translation elongation factor EF-Ts - *Helicobacter pylori* (strain J99)

C;Date: 03-Feb-2003 #sequence\_revision 03-Feb-2003 #text\_change 09-Jul-2004  
 C;Accession: JCT7905  
 R;Kawakami, A.; Yoshida, M.  
 Biosci. Biotechnol. Biochem. 66, 2297-2305, 2002  
 A;Title: Molecular characterization of sucrose:sucrose 1-fructosyltransferase and sucrose  
 A;Accession: JCT7905  
 A;Molecule type: mRNA  
 A;Residues: 1-662 <RAW>  
 A;Cross-references: UNIPROT:Q8W430; DDBJ:AB029888  
 C;Comment: This enzyme, which is a vacuole-type fructosyltransferase and a fructan-biosy-  
 fers a fructosyl moiety from one sucrose to another, resulting in the formation of trisa-  
 C;Genetics:  
 A;Gene: wft2  
 C;Keywords: glycosyltransferase; hexosyltransferase  
  
 Query Match 12.5%; Score 64.5%; DB 2; Length 662;  
 Best Local Similarity 28.8%; Pred. No. 43;  
 Matches 21; Conservative 14; Mismatches 25; Indels 13; Gaps 4;  
  
 QY 5 CLN--VGLIRKLSDPFDPOBGWKKLAVAKKPGGDYRNOFHIRFEALQTGKSPTE 61  
 ::|::|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 320 CIDIAVGGERKASDYNSTA--EDVIVWIKKSSDDDRHDMWISLGKFDAAKWW-TRIDE 376  
 QY 62 -----LLFDWG 67  
 ::|:|||:  
 Db 377 ELELGVGLRKYDWG 389

RESULT 15

GB2217 probable 6-pyruvoyl tetrahydrobiopterin synthase vc1299 [imported] - vibrio cholerae (strain N16961)  
 C;Species: Vibrio cholerae  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: GB2217  
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 chardson, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.  
 L.; R.R.; Mekalanos, J.-J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A;Reference number: A82035; PMID:0946833; PMID:10952301  
 A;Accession: G82217  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-122 <RAW>  
 A;Cross-references: UNIPROT:Q9KSF7; GB:AB004209; GB:AB003852; NID:99655779; PIDN:AAF9445  
 C;Genetics:  
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
 A;Gene: VC1299  
 A;Map position: 1  
 C;Superfamily: 6-pyruvoyl tetrahydropterin synthase

Query Match 12.4%; Score 64; DB 2; Length 122;  
 Best Local Similarity 34.6%; Pred. No. 6.3; Mismatches 8; Indels 8; Gaps 3;  
 Matches 18; Conservative 8; Mismatches 18; Indels 8; Gaps 3;

QY 18 IDPQGKGWKKLAVAIIK---KPSGDDPRNQPHIRRFPEALQTGKSPTEBLFDW 66  
 ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 46 VDPHKGWVWDPAEIKKAQPKPT-YDRDHYWINDIGI---ENPTSEVLAKN 92

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### OM protein - protein search, using sw model

Run on: January 10, 2005, 23:08:19 ; Search time 193 Seconds  
 292.159 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517  
 Sequence: 1 TYVRCVLNGLIRKLSDRIDP.....LLIONEFFAPASLLPDADV 98

Scoring table: BloSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 1825181 seqs, 5753174646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt 02;\*  
 1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	517	100.0	460	1 IRA4 HUMAN
2	513	99.2	218	2 Q7Z6A7
3	513	99.2	292	2 Q7Z6A8
4	476	92.1	197	2 Q9D250
5	476	92.1	459	1 IRA4 MOUSE
6	287	55.5	382	2 Q7ZWW7
7	287	55.5	483	2 Q6IWL3
8	287	55.5	483	2 ART37635
9	98.5	19.1	609	2 Q8CTU8
10	98.5	19.1	609	2 Q8CB40
11	96.5	18.7	596	2 Q9Y616
12	96.5	18.7	596	2 AAH5700
13	96.5	18.7	596	2 AAH69388
14	95	18.4	609	2 Q8KB42
15	88	17.0	296	2 QGY1S1
16	88	17.0	296	2 AAQ91937
17	86	16.6	672	2 Q7ZIE4
18	82	15.9	162	2 Q8CIX0
19	82	15.9	296	1 MY88_MOUSE
20	79	15.3	590	1 IRA2_HUMAN
21	75.5	14.6	257	2 Q34744
22	74.5	14.4	550	2 Q9D1S0
23	74.5	14.4	550	2 Q8VIC0
24	73.5	14.2	539	2 Q6PB60
25	73.5	14.2	539	2 AAH59871
26	72.5	14.0	824	1 MTL1_HUMAN
27	72	13.9	462	1 TUBE_DROME
28	71.5	13.8	562	2 Q8DMT6
29	71.5	13.8	1076	1 HSBR_CAVPO
30	71.5	13.8	5826	2 Q76KYO
31	71.5	13.8	5826	2 BAD08373

### ALIGNMENTS

RESULT 1

ID	IRA4_HUMAN	STANDARD;	PRT;	460 AA.
AC	Q9NNZ3; Q8TDFF7; Q9J5B9;			
DT	01-OCT-2004 (Rel. 45, Created)			
DT	01-OCT-2004 (Rel. 45, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interleukin-1 receptor-associated kinase-4 (EC 2.7.1.-) (IRAK-4) (NY-REN-64 antigen).			
GN	Name=IRAK4;			
OC	Homo sapiens (Human);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.			
OX				

RN [1] R P SEQUENCE FROM N.A., FUNCTION, AND INTERACTIONS WITH IRAK1 AND TRAF6. MEDLINE=1957777; PubMed=11960013; DOI=10.1073/pnas.082100399; R R T IRAK4: A novel member of the IRAK family with the properties of an R R T RAK-kinase."; Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572 (2002). R R R N [2] R P SEQUENCE FROM N.A. MEDLINE=99438124; PubMed=10508479; R R Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H., R R Jongeneel C.V., Gure A.O., Jager D., Knuth A., Chen Y.-T., R R Old L.J.; R R Antigens recognized by autologous antibody in patients with renal R R cell carcinoma"; Int. J. Cancer 83:456-464 (1999). R R R N [3] R P SEQUENCE FROM N.A. R R Pubmed=14702019; DOI=10.1038/ng1285; R R Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., R R Wakamatte A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., R R Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., R R Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., R R Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., R R Shiratori A., Sudo H., Hosoi T., Kaku Y., Koaira H., Kondo H., R R Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa B., R R Omura Y., Abe K., Kamiyama K., Matsuta N., Sato K., Tanikawa M., R R Yamazaki M., Ninomiya K., Ichihashi T., Yamashita H., Murakawa K., R R Fujimori K., Taniai H., Kimata M., Wakabane M., Hirao K., Chiba Y., R R Iida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotoda T., R R Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanabe T.-O., R R Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arata M., R R Imose N., Matsuhashi K., Yuki O., Oshima A., Sasaki N., Notsuka S., R R Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., R R Moriya S., Momiyama H., Satoh M., Takashima Y., Suzuki O., R R Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., R R Hisiigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., R R Yamazaki M., Wattanabe K., Kumagai A., Itakura S., Fukuzumi Y., R R Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., R R Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S., RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., RA Matsunura K., Nakajima Y., Mizuno M., Morinaga M., Sasaki M., RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., RA Okumura K., Nagase T., Nomura H., Kikuchi H., Masuho Y., Yamashita R., RA Nakai K., Yada T., Nakamura Y., Ohara O., Isgai T., Sugano S.; Sugano S., "Complete sequencing and characterization of 21,243 full-length human cDNAs.", Nat. Genet. 36:40-45(2004).

[4] SEQUENCE FROM N.A., AND VARIANTS ARG-98; ARG-390 AND THR-428. Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A., "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)."; RL Submitted (NOV-2002) to the ENSEMBL/GenBank/DDBj databases.

[5] SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derre J.G., Klausner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schaefer G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matsunaga K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., McDonald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Iqbaliano N.A., Betters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McCormick K.J., Malek J.A., Guarnaccia P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gray L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heaton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krawczynski M., Skalka U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marras W.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903 (2002).

RT -!- FUNCTION: Involved in ILK-R-induced NF-kappa-B (NFkB) activation as well as the activation of mitogen-activated protein (MAP) kinase pathways. Phosphorylates IRAK1.

CC -!- SUBUNIT: Interacts with TRAF6 and IRAK1.

CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Pelle subfamily.

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KW	Transferase.
RA	DOMAIN 186 454 Protein kinase.
RA	NP-BIND 192 200 ATP (By similarity).
RA	BINDING 213 213 ATP (By similarity).
RA	ACT SITE 311 311 Proton acceptor (By similarity).
RA	VARIANT 98 98 S -> R. /FTId=VAR_019354.
FT	VARIANT 390 390 H -> R. /FTId=VAR_019355.
FT	VARIANT 428 428 A -> T. /FTId=VAR_019356.
FT	CONFLICT 81 81 U -> A (in Ref. 1). V -> G (in Ref. 2).
FT	CONFLICT 432 432 L -> R (in Ref. 2).
FT	CONFLICT 437 437 R -> S (in Ref. 2).
FT	CONFLICT 444 444 Q -> H (in Ref. 2).
FT	CONFLICT 451 451
SQ	SEQUENCE 460 AA: 51529 MW: 6CB8156ADP25P81E CRC64; Query Match Best Local Similarity 100.0%; Score 517; DB 1; Length 460; Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
ID 0726A7 PRELIMINARY;  
AC 0726A7;  
DT 01-OCT-2003 (TREMBL); 25, Created)

DB 01-MAR-2004 (TREMBL); 25, Last sequence update)

DE Interleukin-1 receptor associated kinase 4 mutant form 2.

GN Name=IRAK4;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI\_TaxID=9606; RN [1]

RP SEQUENCE FROM N.A.

RA Medvedev A.E., Lentschach A., Kuhns D.B., Blanco J.C.G., Salkowski C., Zhang S., Arditii M., Gallin J.I., Voelz S.N.;

RA "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to

RA Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent

RA Bacterial Infections.", J. Exp. Med. 0:0-0 (2003).

DR EMBL; AY83671; AAY57020.1; "

DR GO: GO:0016301; F-kinase activity; IFA.

DR GO: GO:0004872; F-receptor activity; IFA.

KW Kinase; Receptor

SQ SEQUENCE 218 AA; 24257 MW; B42D2896DACPBDFF9 CRC64;

Query Match 1 TYVRCLANGLIRKLSDPDPQEGWKVKAVALKKPSGDDPRMNPFRREALQLQGKSPS 60

DB 9 TYRCLANGLIRKLSDPDPQEGWKVKAVALKKPSGDDPRMNPFRREALQLQGKSPS 68

QY 61 ELLFDWGTTNTCTVGDLLVLDLILLQNEFAPASLLPDAV 98

DB 69 ELLFDWGTTNTCTAGDLVLDLILLQNEFAPASLLPDAV 106

AC 072648; PRELIMINARY; PRT; 292 AA.  
 AC 072648; 2003 (TREMBrel. 25, Last sequence update)  
 AC 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 AC 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DE Interleukin-1 receptor associated kinase 4 mutant form 1.  
 Name=IRAK4;  
 Homo sapiens (Human).  
 BUKARYA; Mettaoxa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 Medvedev A.B., Lentsch A., Kuhns D.B., Blanco J.C.G., Salkowski C.,  
 Zhang S., Arditì M., Gallin J.I., Vogel S.N.;  
 "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to  
 Lipopolysaccharides and Interleukin-1 in a Patient with Recurrent  
 Bacterial Infections";  
 J. Exp. Med. 0:0-0(2003).  
 DR EMBL; AY283670; AAP57089.1; --.  
 DR GO; GO:000524; P:ATP binding; IEA.  
 DR GO; GO:004672; P:protein kinase activity; IEA.  
 DR GO; GO:0004872; F:transferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:005468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 PFAM; PF00669; Kinase\_1.  
 PRODOM; PD00001; Prot\_kinase\_1.  
 PROSITE; PES0011; PROBIN\_KINASE\_DOM; 1.  
 Kinase; Receptor.  
 SEQUENCE 292 AA; 32704 MW; 58F1708A63BD3BES CRC64;  
 RN [6]  
 Query Match 99.2%; Score 513; DB 2; Length 292;  
 Best Local Similarity 99.0%; Pred. No. 2..3e-49; Indels 0; Gaps 0;  
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 TYRCLNGLIRKLSDFDPOEGWKKLAVAIKEPKSGDRYNOFHIRRPEALIOTGKSPS 60  
 Db 9 TYRCLNGLIRKLSDFDPOEGWKKLAVAIKEPKSGDRYNOFHIRRPEALIOTGKSPS 68  
 Qy 61 ELLFDWGTTCTGDLVLDLQNEFFAPASLLPDAVP 98  
 Db 69 ELLFDWGTTCTGDLVLDLQNEFFAPASLLPDAVP 106  
 RESULT 4  
 O9D250 PRELIMINARY; PRT; 197 AA.  
 AC 09D250; 2001 (TREMBrel. 17, Created)  
 AC 09D250; 01-JUN-2001 (TREMBrel. 19, Last sequence update)  
 AC 09D250; 01-DEC-2001 (TREMBrel. 19, Last sequence update)  
 AC 09D250; 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DE Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched  
 library, clone:9330209D03 product:interleukin-1 receptor-associated  
 kinase 4.  
 Name=Irak4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 MEDLINE=99219253; PubMed=0349636;  
 RA Carninci P., Hayashi Y., Sugahara Y., Shibata K., Itoh M.,  
 RA Kanno H., Ozaki Y., Muramatsu M., Hayashizaki Y.;  
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RT Genome Res. 10:1617-1630(2000).  
 RN [5]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 MEDLINE=2049374; PubMed=11042159;  
 RN [4]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 MEDLINE=2050913; PubMed=11076861;  
 RX SHIBATA K., ITOH M., AIZAWA K., NAGAOKA S., SASAKI N., CARNINCI P.,  
 RA KONNO H., AKIYAMA J., NISHI K., KITSUNAI T., TASHIRO H., ITOH M.,  
 RA SUMI N., ISHII Y., NAKAMURA S., HAZAMA M., NISHINE T., HARADA A.,  
 RA YAMAMOTO R., MATSUMOTO H., SAKAGUCHI S., IKEGAMI T., KASHIWAGI K.,  
 RA FUJIWAKE S., INOUE K., TOASA Y., IZAWA M., OHARA E., WATANABE K.,  
 RA YONEDA Y., ISHIKAWA T., OZAWA K., TANAKA T., MATSUURA S., KAWAI J.,  
 RA OKAZAKI Y., MURAMATSU M., INOUE Y., KIRA A., HAYASHIZAKI Y.;  
 RT "RIKEN integrated sequencing pipeline (RISP) system-384-format  
 sequencing pipeline with 384 multicepillary sequencer.";  
 RT Genome Res. 10:1757-1771(2000).  
 RN [6]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
 RA ARAKAWA T., BONO H., CARNINCI P., FUKUDA S., FUKUNISHI Y., ARAI A., AONO H.,  
 RA HIRAMOTO K., HIRAMOTO K., HIRAMOTO K., HIRAMOTO K., HIRAMOTO K.,  
 RA IMOTANI K., ISHII Y., ITOH M., IZAWA M., KASUOYA T., KATO H.,  
 RA KAWAI J., KOJIMA Y., KONNO H., KOURADA M., KOYA S., KURIHARA C.,  
 RA MATSUYAMA T., MIZAKI A., NISHI K., NOMURA K., NUMAZAKI R., OHNO M.,  
 RA OKAZAKI Y., ODO T., OWA C., SITO H., SAITO R., SAKAZI C., SAKAI K.,  
 RA SANO H., SAKAKI D., SHIBATA K., SHIBATA Y., SHINAGAWA A., SHIRAKI T.,  
 RA SOGABE Y., SUZUKI H., TAGAMI M., TAISHAWA A., TAKAHASHI F., TAKAKA T.,  
 RA TEIJIMA Y., TOYA T., YAMAMURA T., YASUNISHI A., YOSIDA K., YOSHINO M.,  
 RA MURAMATSU M., HAYASHIZAKI Y.;  
 DR Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK020397; BAB3090.2; --.  
 DR MGJ; MGJ:2182474; Irak4.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0004972; P:receptor activity; IEA.  
 DR GO; GO:007165; P:signal transduction; IEA.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR01029; DEATH-like.  
 DR Pfam; PP0531; Death; 1.  
 DR Kinase; Receptor.  
 KW SEQUENCE 197 AA; 21695 MW; 142B61EB8A614898 CRC64;  
 Query Match 92.1%; Score 476; DB 2; Length 197;  
 Best Local Similarity 90.8%; Pred. No. 2..2e-45; Indels 0; Gaps 0;  
 Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 TYRCLNGLIRKLSDFDPOEGWKKLAVAIKEPKSGDRYNOFHIRRPEALIOTGKSPS 60  
 Db 9 TYRCLNGLIRKLSDFDPOEGWKKLAVAIKEPKSGDRYNOFHIRRPEALIOTGKSPS 68  
 Qy 61 ELLFDWGTTCTGDLVLDLQNEFFAPASLLPDAVP 98  
 Db 69 ELLFDWGTTCTGDLVLDLQNEFFAPASLLPDAVP 106  
 RESULT 5  
 IR4 MOUSE

ID 08RA4 MOUSE STANDARD; PRT; 459 AA.  
AC Q8RAK2; 080WMI;  
DT 01-OCT-2004 (Rel. 45, Created)  
DT 01-OCT-2004 (Rel. 45, Last sequence update)  
DE Interleukin-1 receptor-associated kinase-4 (BC 2.7.1.-) (IRAK-4).  
GN Mus musculus (Mouse).  
OS Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TAXID=10090;  
RN [1] Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [2] SEQUENCE FROM N.A.  
RP STRAIN=BALB/c;  
RC MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RN [2] SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2234683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami H., Yamakawa I., Kyosawa H.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Battalou S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,  
RA Dalla F., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gabriloidi M., Gibi C., Gozik A., Gough J., Jackson I.J., Jarvis E.D.,  
RA Grimmmond S., Gusinovich S., Hirokawa N., Kanoai A., Kawaji H., Kawasawa Y., Kedański R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Leinwand B., McKenna N., Mikiti H.,  
RA Maglott D.R., Maitaisi L., Marchionni L., McNamee L., Mikiti H.,  
RA Nagashima T., Numata K., Okido T., Pavani W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Reed J.C., Reid J.J., Ringwald M.,  
RA Ravasi T., Reed J.C., Semple C.A., Setou M., Shimada K.,  
RA Sandelin A., Schneider C., Sempel C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teadale D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyrshik Boris A., Yangcissawa M., Yang J., Yang L.,  
RA Yuan Z., Zavolan M., Zhu H., Zimmer A., Cernicci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,  
RA Miyazaki A., Sakai K., Saraki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT full-length cDNAs";  
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RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Skin;  
RA MEDLINE-2195277; PubMed=11960013; DOI=10.1073/pnas.082100399;  
RA LI. S., Strelow A., Fontana E.J., Wesche H.;  
RT "IRAK4: A novel member of the IRAK family with the properties of an  
TRAK-kinase.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).<

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Butewow K.H., Schneider C.F., Bhat N.K.,  
 RA Hsieh F., Go; GO:0016301; F:kinase activity; IEA.  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Carabanti T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshimaru S., Carnicci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards B., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.,  
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Slatka J., Smailus D.E., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=whole body;  
 RA STRASBERG R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDJB databases.  
 EMBL; BC045381; AR#45381\_1; -;  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:004672; F:protein kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO; GO:007165; P:signaling transduction; IEA.  
 DR InterPro; IPR00488; Death.  
 DR InterPro; IPR011029; DEATH like.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW SEQUENCE 382 AA; 41769 MW; 2FD6B572B4CB2B CRC64;  
 Query Match 55.5%; Score 287; DB 2; Length 483;  
 Best Local Similarity 53.7%; Pred. No. 1.4e-23;  
 Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
 Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 TYVRCLANGVGLRKLSDFIDPOBGWKKLAVATAKKPSGDDRNQFHIRRFEEALLQLQTKSPT 60  
 Db 8 TPVKLRLYSALRALADLDPDTWSRIMADISRPGCPRTQMHRRFEACVLUQKSPTM 67  
 QY 61 BLIFDGMGTCTVGDVLVLLQNEPPAPASLILPD 95  
 Db 68 BLIFDWGTSCTVGDVLVLLIRHQFAVTVLILPD 102  
 RESULT 7  
 061W13 PRELIMINARY; PRT; 483 AA.  
 AC Q61W13;  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Interleukin-1 receptor-associated kinase 4.  
 GN Namesirak;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Cyprinidae; Danio.  
 NCBI-TaxID=7955;  
 RN  
 Sequence FROM N.A.  
 RA Phelan P.E., III, Mellon M.T., Kim C.H.;  
 RT "Untitled.";  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDJB databases.  
 EMBL; AR#6584; AR#73635.1; -.  
 DR Kinase; Receptor.  
 KW SEQUENCE 483 AA; 53708 MW; 510BDAC250561F7 CRC64;  
 SQ  
 Query Match 55.5%; Score 287; DB 2; Length 483;  
 Best Local Similarity 53.7%; Pred. No. 1.4e-23;  
 Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
 Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 TYVRCLANGVGLRKLSDFIDPOBGWKKLAVATAKKPSGDDRNQFHIRRFEEALLQLQTKSPT 60  
 Db 8 TPVKLRLYSALRALADLDPDTWSRIMADISRPGCPRTQMHRRFEACVLUQKSPTM 67  
 QY 61 BLIFDGMGTCTVGDVLVLLQNEPPAPASLILPD 95  
 Db 68 BLIFDWGTSCTVGDVLVLLIRHQFAVTVLILPD 102  
 RESULT 9  
 Q8C7UB PRELIMINARY; PRT; 609 AA.  
 AC Q8C7UB;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Phelan P.E., III, Mellon M.T., Kim C.H.;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDJB databases.

DT DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DB Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C30013G03 product:similar to interleukin-1 receptor-associated kinase M, full insert sequence.  
 DE Name=Irak3;  
 OS Mus musculus (Mouse)  
 OC Bokaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Buteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 DR NCBI\_TaxID=10990;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J;  
 RC MEDLINE=9927953; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 Meth. Enzymol. 303:19-44 (1999).  
 [2] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J;  
 RC MEDLINE=2108560; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409:685-690 (2001).  
 [3] SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 Nature 420:563-573 (2002).  
 RN [4] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J;  
 RC MEDLINE=205374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 Genome Res. 10:1617-1630 (2000).  
 RN [5] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J;  
 MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 Konno H., Akimura J., Nishi K., Kitsunari T., Tashiro H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hizawa T., Harada A.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasihagi K.,  
 Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,  
 Yoneya Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis system (RISA) system:384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 Genome Res. 10:1757-1771 (2000).  
 RN [6] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 Hayashiida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 Hori F., Imortani K., Ishii Y., Itoh M., Kagewa I., Kasekawa T.,  
 Kato H., Kawai J., Kohjima Y., Kondo S., Kondo H., Koya S.,  
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 Nishi K., Nomura K., Numazaki K., Ohno M., Ohnoso N., Okazaki Y.,  
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 DR Submitted (JUL-0-2001) to the EMBL/GenBank/DBJ databases.  
 MGD; MGI:1921164; Irak3.

DR GO; GO:0016301; F:kinase activity; IDA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
 DR GO; GO:007165; P:signal transduction; IDA.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH like.  
 DR InterPro; IPR010919; Kinase like.  
 DR InterPro; IPR000119; Prot\_Kinase.  
 PRAM; PR0051; Death; 1.  
 DR PRAM; PR0069; Protein; 1.  
 PRODom; P00001; Prot\_kinase; 1.  
 PROSITE; PS00017; DEATH DOMAIN; 1.  
 DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR KW Kinase; Receptor; PROTEIN\_KINASE\_DOM; 1.  
 SQ SEQUENCE 609 AA; 68425 MW; C8FB51065B2313C4 CRC64;  
 SQ

Query Match 19.1%; Score 98.5; DB 2; Length 609;  
 Best Local Similarity 31.5%; Pred. No. 0.036;  
 Matches 23; Conservative 13; Mismatches 30; Indels 7; Gaps 0

OY 8 VGLIRKUSDPDPQEGWKKLAVAIKKPSSGGDDRYNQHIFRREALIQTGKSPPTSETLFDWG  
 Db 25 IGLIGCGILDSCGPGLGRGLAERLSN-----SMVDYRHIEKVINQKGSGTRELLWSWA

OY 68 TNCTVTDVLVQIL 80  
 Db 78 QKRNKTIGDILEVL 90

RESULT 10  
 O8CE40 PRELIMINARY; PRT; 609 AA.  
 ID O8CE40  
 AC 08CE40; QKLN8;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DE Mus musculus 10 days neonate Skin cDNA, RIKEN full-length enriched  
 library, clone:173286H23 product:similar to interleukin-1 receptor-  
 associated kinase M, full insert sequence (IL-1 receptor-associated  
 kinase M);  
 Name=Irak3; Synonyms=Irak-M;  
 OS Mammalia;  
 OC Bokaryota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Buteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 DR NCBI\_TaxID=10990;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Skin;  
 RC MEDLINE=9927953; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 Meth. Enzymol. 303:19-44 (1999).  
 RN [2] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Skin;  
 RC MEDLINE=208560; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409:685-690 (2001).  
 RN [3] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Skin;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 Nature 420:563-573 (2002).  
 RN [4] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Skin;  
 RA MEDLINE=205374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to



Db 78 QRNKTVGDLQLQVL 90  
 RESULT 12  
 AAH57800 PRELIMINARY; PRT; 595 AA.  
 ID AAH57800;  
 AC AAH57800;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE Interleukin-1 receptor-associated kinase 3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner D., Shemmen C.M., Schuler G.D.,  
 RA Altenschul S.F., Zeeberg B., Buetow K.H., Schacter C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
 RA Diatchenko L., Matsusita K., Farmer A.A., Rubin G.M., Hong J.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Range C.,  
 RA Raha S.S., Loquaiello N.A., Peters G.J., Malek J.A., Gunaratne P.H.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Madan A., Shvchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC069388; AAH69388.1; -.  
 KW Sequence; Receptor;  
 SQ SEQUENCE 596 AA; 67752 MW; E37433EADD7E38BE CRC64;  
 Query Match 18.7%; Score 96.5; DB 2; Length 596;  
 Best Local Similarity 31.5%; Pred. No. 0.058; Mismatches 31; Indels 7; Gaps 1;  
 Matches 23; Conservative 12; MisMatches 31; Del 7; Insert 1;  
 QY 8 VGLIRKLSPFDIPQEGWKKLAVAIKKPGSGDRYNOFHIRRFEALLQTGSKPSPTSELFDWG 67  
 QY 8 VGLIRKLSPFDIPQEGWKKLAVAIKKPGSGDRYNOFHIRRFEALLQTGSKPSPTSELFDWG 67  
 DB 25 LGELCAVLDSCDGAIGWGLAERLSS-----SWLDVHIEKVYDQGKSGTRELLWMA 77  
 QY 68 TNCTCTVGDVLPDL 80  
 DB 78 QRNKTVGDLQLQVL 90  
 RESULT 14  
 Q8K4B2 ID Q8K4B2 PRELIMINARY; PRT; 609 AA.  
 AC Q8K4B2;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Interleukin-1 receptor-associated kinase M.  
 GN Name=Irak3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=2215925; PubMed=12150927;  
 RA Kobayashi K., Hernandez J.D., Galan J.E., Janeway C.A. Jr.,  
 RA Medzhitov R., Flavell R.A.,  
 RT "IRAK-M is a negative regulator of Toll-like receptor signaling.";  
 RL Cell 110:191-200 (2002).  
 DR EMBL; AA461763; NM8393.1; -.  
 DR MGII:1921164; Irak3.  
 GO; GO:0016301; P:kinase activity; IDA.  
 GO; GO:000668; P:protein amino acid phosphorylation; IDA.  
 OC Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DR GO; GO:0007165; P-signal transduction; IDA.  
 DR InterPro; IPR000498; Death.  
 DR InterPro; IPR011059; DEATH like.  
 DR InterPro; IPR011059; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR Pfam; PF00531; Death; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOMAIN; 1.  
 KW Kinase; Receptor.  
 SQ SEQUENCE 609 AA; 68557 MW; 19E4D129FF854DD73 CRC64;  
 Query Match 18.4%; Score 95; DB 2; Length 609;  
 Best Local Similarity 32.4%; Pred. No. 0.059; Gaps 2;  
 Matches 24; Conservative 12; Mismatches 28; Indels 10; Gaps 2;  
 Qy 10 LIRKLUSDFIDPQE--GWKKLAVAIKKRSGDDRYNQFHRRFEALLQKSPRSBELLFW 66  
 Db 24 LGELGIGLSDWDGPGLGWWGLAERLSN-----SWLDVRIIEKVLYNQKGIRELLMSW 76  
 Qy 67 GTRNCTVGDLVLL 80  
 Db 77 AQRKIKTIGDNLIEVL 90

RESULT 15

06Y1S1 PRELIMINARY; PRT; 296 AA.  
 ID 06Y1S1; AC 06Y1S1;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DB Myeloid differentiation primary response gene 88.  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SSQUENCE FROM N.A.  
 RC STRAIN=Mistar; TISSUE=Spleen;  
 RA Li Y., Ji A., Schaefer M.K.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AV191270; AAQ091937.1; -.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR000157; TIR.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF01582; TIR; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00255; TIR; 1.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 DR PROSITE; PS500104; TIR; 1.  
 SQ SEQUENCE 296 AA; 33083 MW; 7A74304BEB61DBCEO CRC64;  
 Query Match 17.0%; Score 88; DB 2; Length 296;  
 Best Local Similarity 35.0%; Pred. No. 0.23; Gaps 4;  
 Matches 28; Conservative 11; Mismatches 25; Indels 16; Gaps 4;  
 Qy 6 LNYGLRKLUISDFIDPQE--EGWKKLAVAIKKRSGDDRYNQFHRRFEALLQKSPRSB 61  
 Db 25 LNVQVRRRLSLFLNPRTTAAADWTSLAEM-----GPEYLEIREPFS---TRPDPTRS 73  
 Qy 62 LILFWW-GTRNCTVGDLVLL 80  
 Db 74 LLDWQGRGSVVERILLELL 93

Search completed: January 10, 2005, 23:25:08  
 Job time : 195 secs

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OM protein - protein search, using sw model  
 Run on: January 10, 2005, 23:16:45 ; Search time 38 Seconds  
 (without alignments)  
 171.031 Million cell updates/sec

Title: US-10-001-254-6  
 Perfect score: 517  
 Sequence: 1 FIVVRLCLNVLIRKNSDFIDP. .... LLIQNEFAPASLILUPDAV 98  
 Scoring table: BLOSUM62  
 Gapopt 10.0 , Gapext 0.5

Searched: 478139 seqs, 63318000 residues

Total number of hits satisfying chosen parameters: 478139  
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Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued Patents AA: \*  
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 6: /cgn2\_6/pctodata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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4	79	15.3	590	2 US-08-980-060-2
5	79	15.3	590	3 US-07-107-183-2
6	79	15.3	590	4 US-09-773-753-2
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8	79	15.3	625	3 US-09-307-183-4
9	79	15.3	625	4 US-09-773-753-4
10	69.5	13.4	398	4 US-09-330-543-20
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13	69.5	13.4	593	3 US-09-234-393-52
14	69.5	13.4	593	3 US-09-234-393-54
15	69.5	13.4	593	4 US-09-865-171-24
16	69.5	13.4	593	4 US-09-825-171-50
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18	69.5	13.4	593	4 US-09-865-171-54
19	69.5	13.4	593	4 US-09-288-393A-50
20	69.5	13.4	593	4 US-09-897-586A-50
21	69.5	13.4	593	4 US-09-895-752-50
22	69.5	13.4	593	4 US-09-903-012B-50
23	69.5	13.4	593	4 US-09-900-797-50
24	66.5	12.9	215	4 US-09-489-039A-12048
25	66	12.8	70	4 US-09-288-796A-21148
26	66	12.8	328	4 US-09-252-991A-27932
27	64.5	12.5	506	3 US-09-134-001C-3307

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RESULT 1
US-09-166-350-21
; Sequence 21, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockett, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILES REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-166-350-21

Query Match          100 0%; Score 517; DB 4; Length 206;
Best Local Similarity 100 0%; Pred. No. 8.7e-64; Gaps 0;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYVRCLVGLIRKLSPIFDPRGKWKLAVALKKPSDDDRYQPHRRPEALIQLQGKSPS 60
Db      9 TYVRCLVGLIRKLSPIFDPRGKWKLAVALKKPSDDDRYQPHRRPEALIQLQGKSPS 68
Qy      61 ELPFDWGTINCTVGDVLDLIONEFFAPASULLPDVVP 98
Db      69 ELPFDWGTINCTVGDVLDLIONEFFAPASULLPDVVP 106

RESULT 2
US-09-135-232-2
; Sequence 2, Application US/09135232
; Patent No. 626228
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: 1998-019
; CURRENT APPLICATION NUMBER: US/09/135,232
; CURRENT FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2

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COMPUTER: IBM PC compatible  
SEQ ID NO 2  
; LENGTH: 596  
; TYPE: PRT  
; ORGANISM: human  
; US-09-135-232-2

Query Match ` 18.7%; Score 96.5; DB 3; Length 596;  
Best Local Similarity 31.5%; Pred. No. 0.0019; 12; Mismatches 31; Indels 7; Gaps 1;  
Matches 23; Conservative 12; MisMatche

RESULT 3  
US-09-863-549-2  
; Sequence 2, Application US/09863549  
; Patent No. 6576444  
; GENERAL INFORMATION:  
; APPLICANT: CAO, Zhaodan  
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods  
; FILE REFERENCE: 798-019  
; CURRENT APPLICATION NUMBER: US/09/863, 549  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 09/135, 232  
; PRIOR FILING DATE: 1998-08-17  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 596  
; TYPE: PRT  
; ORGANISM: human

Query Match 18.7%; Score 96.5; DB 4; Length 596;  
Best Local Similarity 31.5%; Pred. No. 0.00019; 12; Mismatches 31; Indels 7; Gaps 1;  
Matches 23; Conservative 12; MisMatche

RESULT 4  
US-08-980-060-2  
; Sequence 2, Application US/0980060  
; Patent No. 595421  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: FENG, PING  
; APPLICANT: MUZIO, MARTA  
; APPLICANT: DIXIT, VISHVA M.  
; TITLE OF INVENTION: HUMAN IRAK-2  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/307, 185  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/980, 060  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36, 688  
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 590 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

RESULT 5  
US-08-980-060-2  
; Sequence 2, Application US/09307185  
; Patent No. 6222019  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: FENG, PING  
; APPLICANT: MUZIO, MARTA  
; APPLICANT: DIXIT, VISHVA M.  
; TITLE OF INVENTION: HUMAN IRAK-2  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/307, 185  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/980, 060  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36, 688  
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:



ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P. L. L.C.

STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/307,185

FILING DATE: <Unknown>

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/980,060

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 625 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-307-185-4

Query Match 15.3%; Score 79; DB 3; Length 625;  
Best Local Similarity 31.9%; Pred. No. 0.056; Gaps 2;  
Matches 22; Conservative 12; Mismatches 19; Indels 16; Gaps 2;

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 625 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-307-185-4

RESULT 10  
US-09-360-45-20  
; Sequence 20, Application US/09360545  
; Patient No. 6429014

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Bohmian, Jorg

APPLICANT: Steele, Christopher L

APPLICANT: Phillips, Michael A

TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

FILE REFERENCE: WUR13885

CURRENT APPLICATION NUMBER: US/09/360,545

EARLIER APPLICATION NUMBER: 60/052,249

EARLIER FILING DATE: 1997-11-07

EARLIER APPLICATION NUMBER: PCT/US98/14528

EARLIER FILING DATE: 1998-07-10

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 20

LENGTH: 398

TYPE: PRT

ORGANISM: Abies grandis

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Best Local Similarity 31.1%; Pred. No. 0.62; Gaps 10;  
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 625 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-360-45-20

Query Match 13.4%; Score 69.5; DB 4; Length 398;  
Best Local Similarity 31.1%; Pred. No. 0.62; Gaps 10;  
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 625 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-360-45-20

RESULT 11  
US-09-234-393-24  
; Sequence 24 Application US/09234393A  
; Patent No. 6265339  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B  
; APPLICANT: Crock, John E  
; APPLICANT: Bohiman, Jorg  
; APPLICANT: Jetter, Reinhard  
; APPLICANT: Steele, Christopher L  
; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)  
; FILE REFERENCE: WSURL13345  
; CURRENT APPLICATION NUMBER: US/09/234,393A  
; CURRENT FILING DATE: 1999-01-20  
; EARLIER APPLICATION NUMBER: 60/072,204  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 24  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Abies grandis  
; US-09-234-393-24  
Query Match 13.4%; Score 69.5; DB 3; Length 593;  
Best Local Similarity 31.1%; Pred. No. 1.1; Mismatches 41; Indels 41; Gaps 10;  
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;  
Qy 3 VRCIANGVGLIRKLSPID-PQEGWKK---LAVAIIKKSGDD---RYNQFIRRFEAL 51  
Db 362 VRRMDVSIVLEGPLDPFMKIAFEFLUKTSNELLAEV-KAQGQDMAAYIRKNAWE-RYLEAV 419  
Qy 52 LQ----TGKSPTSBLLFDWGTTN---CTVGLDVLQIINE-----FPAP---- 88  
Db 420 LQDAEWIATGHVPTFDEVLYNGIPNTGMCVL-NLIPLLMGEHLPIDILEQIFLPSRFHH 478  
Qy 89 ---ASLLPDA 96  
Db 479 LIELASRLVDDA 490

RESULT 12  
US-09-234-393-50  
; Sequence 50 Application US/09234393A  
; Patent No. 6265339  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B  
; APPLICANT: Crock, John E  
; APPLICANT: Bohiman, Jorg  
; APPLICANT: Jetter, Reinhard  
; APPLICANT: Steele, Christopher L  
; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)  
; FILE REFERENCE: WSURL13345  
; CURRENT APPLICATION NUMBER: US/09/234,393A  
; CURRENT FILING DATE: 1999-01-20  
; EARLIER APPLICATION NUMBER: 60/072,204  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 52  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(817)  
; OTHER INFORMATION: Computer-generated protein sequence  
; US-09-234-393-52  
Query Match 13.4%; Score 69.5; DB 3; Length 593;  
Best Local Similarity 31.1%; Pred. No. 1.1; Mismatches 41; Indels 41; Gaps 10;  
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;  
Qy 3 VRCIANGVGLIRKLSPID-PQEGWKK---LAVAIIKKSGDD---RYNQFIRRFEAL 51  
Db 362 VRRMDVSIVLEGPLDPFMKIAFEFLUKTSNELLAEV-KAQGQDMAAYIRKNAWE-RYLEAV 419  
Qy 52 LQ----TGKSPTSBLLFDWGTTN---CTVGLDVLQIINE-----FPAP---- 88  
Db 420 LQDAEWIATGHVPTFDEVLYNGIPNTGMCVL-NLIPLLMGEHLPIDILEQIFLPSRFHH 478  
Qy 89 ---ASLLPDA 96  
Db 479 LIELASRLVDDA 490

RESULT 13  
US-09-234-393-52  
; Sequence 52 Application US/09234393A  
; Patent No. 6265339  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B  
; APPLICANT: Crock, John E  
; APPLICANT: Bohiman, Jorg  
; APPLICANT: Jetter, Reinhard  
; APPLICANT: Steele, Christopher L  
; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)  
; FILE REFERENCE: WSURL13345  
; CURRENT APPLICATION NUMBER: US/09/234,393A  
; CURRENT FILING DATE: 1999-01-20  
; EARLIER APPLICATION NUMBER: 60/072,204  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 52  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(817)  
; OTHER INFORMATION: Computer-generated protein sequence  
; US-09-234-393-52  
Query Match 13.4%; Score 69.5; DB 3; Length 593;  
Best Local Similarity 31.1%; Pred. No. 1.1; Mismatches 41; Indels 41; Gaps 10;  
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;  
Qy 3 VRCIANGVGLIRKLSPID-PQEGWKK---LAVAIIKKSGDD---RYNQFIRRFEAL 51  
Db 362 VRRMDVSIVLEGPLDPFMKIAFEFLUKTSNELLAEV-KAQGQDMAAYIRKNAWE-RYLEAV 419  
Qy 52 LQ----TGKSPTSBLLFDWGTTN---CTVGLDVLQIINE-----FPAP---- 88  
Db 420 LQDAEWIATGHVPTFDEVLYNGIPNTGMCVL-NLIPLLMGEHLPIDILEQIFLPSRFHH 478  
Qy 89 ---ASLLPDA 96  
Db 479 LIELASRLVDDA 490

RESULT 14  
US-09-234-393-54  
; Sequence 54 Application US/09234393A  
; Patent No. 6265339  
; GENERAL INFORMATION:

Page 9

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; APPLICANT: Croteau, Rodney B
; APPLICANT: Crock, John E
; APPLICANT: Bohmann, Jorg
; APPLICANT: Jetter, Reinhard
; APPLICANT: Steele, Christopher L
; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: WSUR113345
; CURRENT APPLICATION NUMBER: US/09/234,393A
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 60/072,204
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 54
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(817)
; OTHER INFORMATION: Computer-generated protein sequence
; US-09-234-393-54

Query Match          13.4%; Score 69.5; DB 3; Length 593;
Best Local Similarity 31.1%; Pred. No. 1,1; Mismatches 37; Indels 41; Gaps 10;
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;
QY          3 VRCANGVGLIRKLSDPFDIPOEGWKK-----LAVRIKPSGDD----RYNQHFRFAL 51
OY          3 VRCANGVGLIRKLSDPFDIPOEGWKK-----LAVRIKPSGDD----RYNQHFRFAL 51
Db          362 VRMRWDVSLVLEGIPDFMKIAFEFLWKLTKSNELIAAV-KAQGQDMAVYIRKNAWE-RYLEAY 419
QY          52 LO-----TGKSPTSELFIDWGTTN--CTVGDIVDULIJQNE-----FPAP----- 88
Db          420 LQDREWIAWTCHVPFDEVLININGTNTGCVL-NLPIPLMGENHRIDLEQFLPSRFH 478
QY          89 ----ASLLPDA 96
Db          479 LIELASRLVUDA 490

Db

RESULT 15
US-09-865-171-24
; Sequence 24, Application US/09865171
; Patient No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Crock, John E
; APPLICANT: Bohmann, Jorg
; APPLICANT: Steele, Christopher L
; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
; FILE REFERENCE: WSUR117468
; CURRENT APPLICATION NUMBER: US/09/865,171
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/234,393
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/072,204
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 24
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Abies grandis

Query Match          13.4%; Score 69.5; DB 4; Length 593;
Best Local Similarity 31.1%; Pred. No. 1,1; Mismatches 37; Indels 41; Gaps 10;
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

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GenCore version 5.1.6

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 243.699 Million cell updates/sec

Title: US-10-001-254-6  
 Perfect score: 517  
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 Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
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 20: /cggn2\_6/pctodata/1/pubpaas/usgo\_PUBCOMB\_pep:

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	517	100.0	98	14 US-10-001-254-6
2	517	100.0	460	14 US-10-001-254-16
3	517	100.0	460	14 US-10-001-254-28
4	513	99.2	460	9 US-09-795-595-1
5	513	99.2	460	10 US-09-795-595-1
6	476	92.1	459	9 US-09-795-595-3
7	476	92.1	459	10 US-09-795-595-3
8	247	47.8	59	14 US-10-001-254-26
9	96.5	18.7	596	9 US-09-863-549-2
10	96.5	18.7	644	15 US-10-425-114-54258
11	95	18.4	609	14 US-10-340-545-2
12	79	15.3	590	9 US-09-773-753-2
13	79	15.3	590	14 US-10-366-288-20

RESULT 1	
US-10-001-254-6	
; Sequence 6, Application US/10001254	
; Publication No. US20030049702A1	
; GENERAL INFORMATION:	
; APPLICANT: Reed, John C.	
; APPLICANT: Godzik, Adam	
; APPLICANT: Krysztof	
; APPLICANT: Fiorentino, Loredana	
; APPLICANT: Lee, Sung Hyung	
; APPLICANT: Roth, Wilfried	
; APPLICANT: Steiner-Liwen, Frank	
; TITLE OF INVENTION: No. US20030049702A1 eL Death Domain Proteins	
; FILE REFERENCE: P-LJ 5037	
; CURRENT APPLICATION NUMBER: US10/001,254	
; CURRENT FILING DATE: 2001-11-15	
; PRIOR APPLICATION NUMBER: 60/301,889	
; PRIOR FILING DATE: 2001-06-29	
; PRIOR APPLICATION NUMBER: 09/115,893	
; NUMBER OF SEQ ID NOS: 62	
; SOFTWARE: FastSEQ For Windows Version 4.0	
; SEQ ID NO: 6	
; LENGTH: 98	
; TYPE: PRT	
; ORGANISM: Homo sapien	
US-10-001-254-6	
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Best Local Similarity	100.0%
Matches	98
Conservative	0
Mismatches	0
Indels	0
Gaps	0
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QY 61 ELLFDWGTTCTVGLDVLIDIONEFPAPASLLDAVP 98  
Db 61 ELLFDWGTTCTVGLDVLIDIONEFPAPASLLDAVP 98

RESULT 2  
US-10-001-254-16  
; Sequence 16, Application US/10001254  
; Publication No. US20030049702A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loreadna  
; APPLICANT: Lee, Sug Hyung  
; APPLICANT: Stemer-Liewen, Frank  
; APPLICANT: Roth, Wilfred

TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins

FILE REFERENCE: P-LJ 5037 ; Sequence 1, Application US/10001254  
CURRENT APPLICATION NUMBER: US/10/001, 254  
CURRENT FILING DATE: 2001-11-15  
PRIORITY APPLICATION NUMBER: 60/301, 889  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/715, 893  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 460  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-001-254-16

Query Match 100.0%; Score 517; DB 14; Length 460;  
Best Local Similarity 100.0%; Pred. No. 3; 3e-56;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYVRCLANGLIRKLSDFTDPOEGWKKLAVAIKKPSGDDRYNQFHIRREALQTGKSPS 60  
Db 9 TYVRCLANGLIRKLSDFTDPOEGWKKLAVAIKKPSGDDRYNQFHIRREALQTGKSPS 68

QY 61 ELLFDWGTTCTVGLDVLIDIONEFPAPASLLDAVP 98  
Db 69 ELLFDWGTTCTVGLDVLIDIONEFPAPASLLDAVP 106

RESULT 3  
US-10-001-254-28  
; Sequence 28, Application US/10001254  
; Publication No. US20030049702A1

GENERAL INFORMATION:  
; APPLICANT: John C.  
; APPLICANT: Reed, John C.  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loreadna  
; APPLICANT: Lee, Sug Hyung  
; APPLICANT: Roth, Wilfred

TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins

FILE REFERENCE: P-LJ 5037 ; Sequence 1, Application US/10001254  
CURRENT APPLICATION NUMBER: US/10/001, 254  
CURRENT FILING DATE: 2001-11-15  
PRIORITY APPLICATION NUMBER: 60/301, 889  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/715, 893  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 460  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-001-254-28

RESULT 4  
US-09-795-595-1  
; Sequence 1, Application US/09795595  
; Publication No. US20020039433A1  
; GENERAL INFORMATION:  
; APPLICANT: Wesche, Holger  
; APPLICANT: Li, Shiyun  
; APPLICANT: Tularik Inc.  
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
FILE REFERENCE: 018781-003910US ; Sequence 1, Application US/09795595  
CURRENT APPLICATION NUMBER: US/09/795, 595  
CURRENT FILING DATE: 2001-01-11  
PRIORITY APPLICATION NUMBER: US 60/176, 395  
PRIOR FILING DATE: 2000-01-13  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 460  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-795-595-1

Query Match 100.0%; Score 517; DB 14; Length 460;  
Best Local Similarity 100.0%; Pred. No. 3; 3e-56;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYVRCLANGLIRKLSDFTDPOEGWKKLAVAIKKPSGDDRYNQFHIRREALQTGKSPS 60  
Db 9 TYVRCLANGLIRKLSDFTDPOEGWKKLAVAIKKPSGDDRYNQFHIRREALQTGKSPS 68

QY 61 ELLFDWGTTCTVGLDVLIDIONEFPAPASLLDAVP 98  
Db 69 ELLFDWGTTCTVGLDVLIDIONEFPAPASLLDAVP 106

RESULT 5  
US-09-759-595-1  
; Sequence 1, Application US/09795595  
; Publication No. US20020059916A1  
; GENERAL INFORMATION:  
; APPLICANT: Wesche, Holger  
; APPLICANT: Li, Shiyun  
; APPLICANT: Tularik Inc.  
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
FILE REFERENCE: 018781-003910US ; Sequence 1, Application US/09795595  
CURRENT APPLICATION NUMBER: US/09/795, 595  
CURRENT FILING DATE: 2001-01-13  
PRIORITY APPLICATION NUMBER: US 60/176, 395  
PRIOR FILING DATE: 2000-01-13  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 460  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-595-1

Query Match 99.2%; Score 513; DB 10; Length 460;  
Best Local Similarity 99.0%; Pred. No. 1.1e-55;





FILE REFERENCE: MP102-035P1RNMNIM  
 FILE OF INVENTION: 6747-1793, 1784 OR 2045 MOLECULES  
 CURRENT APPLICATION NUMBER: US/10/366,288  
 CURRENT FILING DATE: 2003-02-13  
 PRIORITY FILING DATE: 2002-02-15  
 PRIORITY APPLICATION NUMBER: 60/380,249  
 PRIORITY FILING DATE: 2002-05-13  
 PRIORITY APPLICATION NUMBER: 60/391,306  
 PRIORITY FILING DATE: 2002-06-25  
 PRIORITY APPLICATION NUMBER: 60/406,297  
 PRIORITY FILING DATE: 2002-08-27  
 PRIORITY APPLICATION NUMBER: 60/412,007  
 PRIORITY FILING DATE: 2002-09-19  
 PRIORITY APPLICATION NUMBER: 60/417,508  
 PRIORITY FILING DATE: 2002-10-10  
 PRIORITY APPLICATION NUMBER: 60/432,318  
 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO: 20  
 LENGTH: 590  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 IS-10-366-288-20

Query Match 15.3%; Score 79; DB 14; Length 590;  
 Best Local Similarity 31.9%; Pred. No. 0.89; Matches 22; Conservative 12; Mismatches 19; Indels 16; Gaps 2;

Qy 45 IRRFEEALQT-GKSPTSEELFDWGTTCTYGGDVLILLQNFFAPASLL----- 93  
 Db 42 LRIKIKSMERVGQSITRELLWWGMQRATVQQLVLDLCLRLYRAAQIILNWKPABIRC 101

Qy 94 ----PDAV 97  
 Db 102 PIPAFPDPSV 110

RESULT 14  
 Sequence 2, Application US/10657146  
 Publication No. US20040110926A1

GENERAL INFORMATION:  
 APPLICANT: NI, JIAN  
 FENG, PING  
 MUZIO, MARTA  
 DIXIT, VISHVA M.  
 TITLE OF INVENTION: HUMAN IRAK-2  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/773,753  
 FILING DATE: 02-Feb-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/980,060  
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK

TELECOMMUNICATION INFORMATION:  
 TELEFAX: (202) 371-2540  
 TELEPHONE: (202) 371-2600

INFORMATION FOR SEQ ID NO: 4  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 625 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4  
 US-09-773-753-4

Query Match 15.3%; Score 79; DB 9; Length 625;  
 Best Local Similarity 31.9%; Pred. No. 0.96;

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEX/FAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 590 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-657-146-2

Query Match 15.3%; Score 79; DB 16; Length 590;  
 Best Local Similarity 31.9%; Pred. No. 0.89; Matches 22; Conservative 12; Mismatches 19; Indels 16; Gaps 2;

Qy 45 IRRFEALQT-GKSPTSEELFDWGTTCTYGGDVLILLQNFFAPASLL----- 93  
 Db 42 LRIKIKSMERVGQSITRELLWWGMQRATVQQLVLDLCLRLYRAAQIILNWKPABIRC 101

Qy 94 ----PDAV 97  
 Db 102 PIPAFPDPSV 110

RESULT 15  
 Sequence 4, Application US/09773753  
 Patent No. US2002009917A1

GENERAL INFORMATION:  
 APPLICANT: NI, JIAN  
 FENG, PING  
 MUZIO, MARTA  
 DIXIT, VISHVA M.  
 TITLE OF INVENTION: HUMAN IRAK-2  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/773,753  
 FILING DATE: 02-Feb-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/980,060  
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK

TELECOMMUNICATION INFORMATION:  
 TELEFAX: (202) 371-2540  
 TELEPHONE: (202) 371-2600

INFORMATION FOR SEQ ID NO: 4  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 625 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-773-753-4

Thu Jan 13 09:24:15 2005

usb-10-001-254-6.rapb

Page 6

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Db	42	IRKIKSMERVQGVSITRELLWWGMRQATVQQLVDLICRLELYRAQIILWWKPAPEIRC								101
QY	94	-----PDAV		97						
Db	102	PIPAFFPSV		110						

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Job time : 146 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: January 12, 2005, 08:09:24 ; Search time 465 Seconds  
 (without alignments)  
 1210.961 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517  
 Sequence: TYVRCLVNLIRKLSDLFDIDP.....LLIONEFFAPASLLLPDAVP 98

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 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 287294193 residues

Total number of hits satisfying chosen parameters: 8600550  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-LOOPCT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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 2: /cgn2\_6/podata/1/pubpna/PCT\_NEW\_PUB.seq:\*
 3: /cgn2\_6/podata/1/pubpna/US06\_PUBCOMB.seq:\*
 4: /cgn2\_6/podata/1/pubpna/US07\_NEW\_PUB.seq:\*
 5: /cgn2\_6/podata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
 6: /cgn2\_6/podata/1/pubpna/US08\_PUBCOMB.seq:\*
 7: /cgn2\_6/podata/1/pubpna/US09\_PUBCOMB.seq:\*
 8: /cgn2\_6/podata/1/pubpna/US09A\_PUBCOMB.seq:\*
 9: /cgn2\_6/podata/1/pubpna/US09B\_PUBCOMB.seq:\*
 10: /cgn2\_6/podata/1/pubpna/US09C\_PUBCOMB.seq:\*
 11: /cgn2\_6/podata/1/pubpna/US09\_NEW\_PUB.seq:\*
 12: /cgn2\_6/podata/1/pubpna/US10\_PUBCOMB.seq:\*
 13: /cgn2\_6/podata/1/pubpna/US10A\_PUBCOMB.seq:\*
 14: /cgn2\_6/podata/1/pubpna/US10B\_PUBCOMB.seq:\*
 15: /cgn2\_6/podata/1/pubpna/US10C\_PUBCOMB.seq:\*
 16: /cgn2\_6/podata/1/pubpna/US10D\_PUBCOMB.seq:\*
 17: /cgn2\_6/podata/1/pubpna/US10E\_PUBCOMB.seq:\*
 18: /cgn2\_6/podata/1/pubpna/US10\_NEW\_PUB.seq:\*
 19: /cgn2\_6/podata/1/pubpna/US11\_NEW\_PUB.seq:\*
 20: /cgn2\_6/podata/1/pubpna/US60\_NEW\_PUB.seq:\*
 21: /cgn2\_6/podata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	294	14 US-10-001-254-5	Sequence 5, Appli
2	517	100.0	1383	14 US-10-001-254-15	Sequence 15, Appli
3	517	100.0	2817	10 US-09-956-451-3	Sequence 3, Appli
4	517	100.0	2817	14 US-10-001-254-27	Sequence 21, Appli
5	517	100.0	2817	16 US-10-001-254-33	Sequence 2, Appli
6	513	99.2	1383	9 US-09-795-595-2	Sequence 2, Appli
7	513	99.2	1383	10 US-09-795-595-2	Sequence 4, Appli
8	476	92.1	1542	9 US-09-795-595-4	Sequence 4, Appli
9	476	92.1	1542	10 US-09-795-595-4	Sequence 14, Appli
10	413	79.9	501	9 US-09-837-790-149	Sequence 10, Appli
11	256	49.5	31000	10 US-09-966-451-10	Sequence 10, Appli
12	256	49.5	31000	15 US-10-630-399-10	Sequence 10, Appli
13	247	47.8	211	14 US-10-001-254-25	Sequence 25, Appli
14	247	47.8	470	16 US-10-242-532A-26096	Sequence 26096, A
15	247	47.8	470	16 US-10-242-532A-26096	Sequence 428, Appli
16	134.5	26.0	408	11 US-09-969-034-428	Sequence 1, Appli
17	96.5	18.7	2288	9 US-09-863-549-1	Sequence 3, Appli
18	96.5	18.7	2293	13 US-10-038-841-3	Sequence 26259, A
19	96.5	18.7	2406	16 US-10-425-11A-26259	Sequence 1, Appli
20	95	18.4	1888	15 US-10-330-541-1	Sequence 1432, Appli
21	95	18.4	1888	14 US-10-188-841-1432	Sequence 19, Appli
22	79	15.3	1782	15 US-10-366-288-19	Sequence 1, Appli
23	79	15.3	1806	9 US-09-773-753-1	Sequence 3, Appli
24	79	15.3	1805	17 US-10-637-141-1	Sequence 3, Appli
25	79	15.3	3459	9 US-09-773-753-3	Sequence 3, Appli
26	79	15.3	3459	17 US-10-637-146-3	Sequence 1432, Appli
27	78.5	15.2	479	9 US-09-773-753-14	Sequence 14, Appli
28	78.5	15.2	479	17 US-10-657-146-14	Sequence 384, Appli
29	78.5	15.2	708	16 US-10-424-599-384	Sequence 3589, Appli
30	78.5	15.2	861	9 US-09-764-877-3589	Sequence 3589, Appli
31	78.5	15.2	861	16 US-10-242-515-3589	Sequence 3589, Appli
32	78.5	15.2	864	9 US-09-764-877-3589	Sequence 3589, Appli
33	78.5	15.2	864	9 US-09-764-877-3589	Sequence 3589, Appli
34	78.5	15.2	864	16 US-10-242-515-3587	Sequence 3587, Appli
35	78.5	15.2	864	16 US-10-242-515-3590	Sequence 3590, Appli
36	75.5	14.6	3128	16 US-10-108-260A-709	Sequence 709, Appli
37	74.5	14.4	774	9 US-09-975-350-1011	Sequence 1011, Appli
38	73.5	14.2	1153	17 US-10-437-963-83917	Sequence 83917, A
39	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
40	73	14.1	497	13 US-10-027-632-50724	Sequence 50724, A
41	73	14.1	497	15 US-10-027-632-50723	Sequence 50723, A
42	73	14.1	497	15 US-10-027-632-50724	Sequence 50724, A
43	73	14.1	499	13 US-10-027-632-72567	Sequence 72567, A
44	73	14.1	499	13 US-10-027-632-72567	Sequence 72567, A
45	73	14.1	499	15 US-10-027-632-72567	Sequence 72567, A

## ALIGNMENTS

RESULT 1

US-10-001-254-5

Sequence 5, Application US/1001254  
 Publication No. US20030049702A1  
 GENERAL INFORMATION:

APPLICANT: Reed, John C.  
 APPLICANT: Gozik, Adam  
 APPLICANT: Pawlowski, Krzysztof  
 APPLICANT: Florentino, Loredana  
 APPLICANT: Lee, Sug Hyung  
 APPLICANT: Roth, Wilfred  
 APPLICANT: Steiner-Lieven, Frank

TITLE OF INVENTION: No. US20030049702A1 eL Death Domain Proteins

FILE REFERENCE: P-LJ 5037

CURRENT APPLICATION NUMBER: US/10/001,254

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 601301,889

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/715,893

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5 LENGTH: 294  
; TYPE: DNA ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS LOCATION: (1) ... (294)  
; US-10-001-254-5

Alignment Scores:  
Pred. No.: 2.69e-71 Length: 294 Score:  
Score: 517.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indexes: 0  
DB: 14 Gaps: 0

US-10-001-254-6 (1-98) x US-10-001-254-5 (1-294)

QY 1 ThryTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAsPro 20  
Db 1 ACATATGCGCCGCTCAATGTTGACTTAATTAGAACCTTGTCAGATTATGATCT 84  
QY 21 GlngLuglyTrpIlysLysLeuAlaValAlaIleLysIleProArgLysAspArgTyr 40  
Db 61 CAAGAGGATGGAAAGAATGCTGTAGCTTAAACCATCTGGATGATGATGATAC 144  
QY 41 AsnGlnPheHisIleArgPheGluAlaLeuIleGlnThrGlyLysSerProThrSer 60  
Db 121 AATCAGTTTCACTAGGAGTTGAGCTTACTTCAACTGGAAAAGTCCACTCT 180  
QY 61 GluleuLeuPheAspTgIlyTrhThrAsnCysTrhValGlyAspLeuValLeu 80  
Db 181 GAAATCTGTTTCACTGGCCACAAATGCAAGTGGTGTGATCTTG 240  
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98  
Db 241 ARCCAAATGAAATTGCTTCGAGCTTGTGCCAGATGCTGTC 294

RESULT 2  
US-10-001-254-15  
; Sequence 15, Application US/10001254  
; Publication No. US20030049702A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Piorrentino, Lorendana  
; APPLICANT: Lee, Sung Hyung  
; APPLICANT: Roth, Wilfried  
; APPLICANT: Stemer-Wenew, Frank  
; TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins  
; FILE REFERENCE: P-LJ 5 037.  
; CURRENT APPLICATION NUMBER: US/10/001-254  
; CURRENT FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 3 LENGTH: 2817

Alignment Scores:  
Pred. No.: 6.87e-70 Length: 2817 Score:  
Score: 517.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indexes: 0  
DB: 10 Gaps: 0

US-10-001-254-6 (1-98) x US-09-966-451-3 (1-2817)

QY 1 ThryTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAsPro 20  
Db 74 ACATATGCGCCGCTCAATGTTGACTTAATTAGAACCTTGTCAGATTATGATCT 133  
QY 21 GlngLuglyTrpIlysLysLeuAlaValAlaIleLysIleProArgLysAspArgTyr 40  
Db 134 CAAGAGGATGGAAAGAATGCTGTAGCTTAAACCATCTGGATGATGATAC 193  
QY 41 AsnGlnPheHisIleArgPheGluAlaLeuIleGlnThrGlyLysSerProThrSer 60  
Db 194 AATCAGTTTCACTAGGAGTTGAGCATTTCAACTGGAAAAGTCCACTCT 253  
QY 61 GluleuLeuPheAspTgIlyTrhThrAsnCysTrhValGlyAspLeuValLeu 80

Alignment Scores:  
Pred. No.: 2.48e-70 Length: 1383

RESULT 4  
US-10-001-254-27

; Sequence 27, Application US/10001254  
; Publication No. US20030049702A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loreddana  
; APPLICANT: Lee, Sug Hyun  
; APPLICANT: Roth, Wilfried  
; APPLICANT: Stenner-Liswen, Frank  
TITLE OF INVENTION: No. US20030049702A1 e1 Death Domain Proteins  
FILE REFERENCE: P-LJ 5037  
CURRENT APPLICATION NUMBER: US/10/001,254  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/3301,889  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/715,893  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 88  
SEQ ID NO 27  
LENGTH: 2817  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (50)...(1432)  
US-10-630-399-3  
Alignment Scores:  
Pred. No.: 6.87e-70 Length: 2817  
Score: 517.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB:  
US-10-001-254-27  
Alignment Scores:  
Pred. No.: 6.87e-70 Length: 2817  
Score: 517.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB:  
US-10-001-254-6 (1-98) x US-10-630-399-3 (1-2817)  
QY 1 ThryTyValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
Db 74 ACATATGGCGCGCTCAATGTTGACTAATTAGGAAGCTGTCAGATTATGATCT 133  
QY 21 GlngGluGlyTrpLysSleuAlaValAlaLysLysProSerGlyAspPargArgTyr 40  
Db 134 CGAGAAGATGGAGAGTGAGTTGACTTAAACCATCTGGTGTAGTAGATAC 193  
QY 41 AspGlnPhasIleArgArgPhagLualLeuIeugLihGlyLysSerProThrSer 60  
DB: 14 Gaps: 0  
US-10-001-254-6 (1-98) x US-10-001-254-27 (1-2817)  
QY 1 ThryTyValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
Db 74 ACATATGGCGCGCTCAATGTTGACTAATTAGGAAGCTGTCAGATTATGATCT 133  
QY 21 GlngGluGlyTrpLysSleuAlaValAlaLysLysProSerGlyAspPargArgTyr 40  
Db 134 CGAGAAGATGGAGAGTGAGTTGACTTAAACCATCTGGTGTAGTAGATAC 193  
QY 41 AspGlnPhasIleArgArgPhagLualLeuIeugLihGlyLysSerProThrSer 60  
Db 194 ATCAGTTTCACATAGGAGATTTGAGCATTTACATCAACTGGAAACGTCCTCT 253  
QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
Db 254 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGCTCTGGAGTCCTTG 313  
QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
Db 254 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGCTCTGGAGTCCTTG 313  
QY 81 IleGluAsnGluPhePheAlaProAlaSerLeuLeuIleAspPheAlaValPro 98  
Db 314 ATCCAAATGATTITGCTCTGGAGTCCTTGCTCCAGATGCTGTCCC 367  
RESULT 5  
US-10-630-399-3  
; Sequence 3, Application US/10630399  
; Publication No. US20040019009A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett

RESULT 6  
US-09-795-595-2

; Sequence 2, Application US/09795595  
; Publication No. US20020039423A1  
; GENERAL INFORMATION:  
; APPLICANT: Wesche, Holger  
; APPLICANT: Li, Shyun  
; APPLICANT: Tularik Inc.  
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
FILE REFERENCE: 018781-003910US  
CURRENT APPLICATION NUMBER: US/09/795,595  
CURRENT FILING DATE: 2001-01-11  
PRIOR APPLICATION NUMBER: US 60/176,395  
PRIOR FILING DATE: 2000-01-13  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 1383  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (RAK-4)  
NAME/KEY: cDNA  
LOCATION: (1)...(1383)  
OTHER INFORMATION: human IRAK-4

US-09-795-595-2

Alignment Scores: 1.05e-69 Length: 1383  
 Pred. No.: 513.00 Matches: 97  
 Score: 98.98% Conservative: 0  
 Percent Similarity: 98.98% Mismatches: 1  
 Best Local Similarity: 98.98% Indels: 0  
 Query Match: 99.23% Gaps: 0  
 DB: US-10-001-254-6 (1-98) x US-09-795-595-2 (1-1383)

QY 1 ThRTyValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPhelleAspPro 20  
 Db 25 ACTATGGCTGCCTCACTTGGCTAAATTAGGAACGTGTCAGATTATGCCCT 84  
 QY 21 GlngLuglyTrpLysLeuAlaValAlaIleLysProSerGlyAspArgTyr 40  
 Db 85 CAAGAACGATGGAAAGAAGTTGAGTTGAGCTTAAACCATCTGGATGATGATAC 144  
 QY 41 AspGlnPheHisIleArgArgPheGluAlaLeuLeuIleArgLysSerProThrSer 60  
 Db 41 AspGlnPheHisIleArgArgPheGluAlaLeuLeuIleArgLysSerProThrSer 60  
 QY 25 AATCAGTTGCGCTCTCATGTTAGGATTTGAGCTTGAGTTGAGCTTAAACCATCTGGATGATGATAC 144  
 QY 21 GlngLuglyTrpLysLeuAlaValAlaIleLysProSerGlyAspArgTyr 40  
 Db 145 AATCAGTTCACATAACGAGTTGAGCTACTTAACTGAAAGTCCACTCT 204  
 QY 61 GluLeuIlePheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
 Db 61 GluLeuIlePheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
 QY 41 AspGlnPheHisIleArgArgPheGluAlaLeuLeuIleArgLysSerProThrSer 60  
 Db 205 GAATTCGTTGACTGGCCACAAATTGCACTGCTGAGCTTGAGCTTGTGCTTC 264  
 QY 81 IleGlnAsnGluPheAspAlaProAlaSerLeuLeuIleProAspAlaValPro 98  
 Db 81 IleGlnAsnGluPheAspAlaProAlaSerLeuLeuIleProAspAlaValPro 98  
 QY 205 GAATTCGTTGACTGGCCACAAATTGCACTGCTGAGCTTGAGCTTGTGCTTC 264  
 Db 265 ATCCAATGAAATTTCGCTGAGCTTGTGCCAGATCGCTGTC 318  
 RESULT 7

US-09-759-595-2

; Sequence 2, Application US/09759595  
; Publication No. US003005991611

; GENERAL INFORMATION:

; APPLICANT: Wesche, Holger  
; APPLICANT: Li, Shyun  
; APPLICANT: Tulark Inc.  
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
; FILE REFERENCE: 018781-003910US  
; CURRENT APPLICATION NUMBER: US/09/795,595  
; CURRENT FILING DATE: 2001-01-11  
; PRIORITY APPLICATION NUMBER: US 60/176,395  
; PRIORITY FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 4  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)  
; NAME/KEY: CDS  
; LOCATION: (163)..(1542)  
; OTHER INFORMATION: murine IRAK-4  
; US-09-795-595-4

Alignment Scores: 7.87e-64 Length: 1542  
 Pred. No.: 476.00 Matches: 89  
 Score: 95.92% Conservative: 5  
 Percent Similarity: 90.82% Mismatches: 4  
 Best Local Similarity: 92.07% Indels: 0  
 Query Match: 92.07% Gaps: 0  
 DB: US-10-001-254-6 (1-98) x US-09-795-595-4 (1-1542)

QY 1 ThRTyValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPhelleAspPro 20  
 Db 247 CAGAAAGGTGGAGAGATTCAGTAGCTCATGAAAGCCGGACGAGATAC 306  
 QY 41 AspGlnPheHisIleArgArgPheGluAlaLeuLeuIleArgLysSerProThrSer 60  
 Db 307 AATCAGTTCCATATAGGAGATTCGAGCCATTACAGCAGCCACCGGT 366  
 QY 61 GluLeuIlePheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
 Db 367 GAACCTGTTGACTGGCCACACGAACTGCACTGCGACGTTGGATCTGTG 426  
 QY 81 IleGlnAsnGluPheAspAlaProAlaSerLeuLeuIleProAspAlaValPro 98  
 QY 1 ThRTyValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPhelleAspPro 20

Db 427 GTCCAGATGAGCTTGGCGGACTCTCCCTGGATGCCCTCCC 480  
**RESULT 9**  
 Publication No. US20030059916A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wesche, Holger  
 ; APPLICANT: Li, Shyun  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
 FILE REFERENCE: 0181-003910US  
 CURRENT APPLICATION NUMBER: US/09/833,790  
 ; PRIORITY FILING DATE: 2001-01-13  
 ; PRIORITY APPLICATION NUMBER: US 60/176,395  
 ; NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 1542  
 TYPE: DNA  
 ORGANISM: Mus sp.  
 FEATURE:  
 OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)  
 OTHER INFORMATION: CDS  
 NAME/KEY: CDS  
 LOCATION: (163)..(1542)  
 OTHER INFORMATION: murine IRAK-4  
 DB:  
 Alignment Scores:  
 Pred. No.: 7.87e-64 Length: 1542  
 Score: 476.00 Matches: 89  
 Percent Similarity: 95.92% Conservative: 5  
 Best Local Similarity: 9.82% Mismatches: 4  
 Query Match: 92.07% Deletions: 4  
 DB: Gaps: 0  
 US-09-759-595-4  
 Alignment Scores:  
 Pred. No.: 1.21e-54 Length: 501  
 Score: 413.00 Matches: 93  
 Percent Similarity: 94.00% Conservative: 1  
 Best Local Similarity: 93.00% Mismatches: 4  
 Query Match: 79.88% Deletions: 4  
 DB: Gaps: 0  
 US-10-001-254-6 (1-98) x US-09-833-790-149 (1-501)  
 QY 1 ThrryValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
 Db 45 ACATATGCGCGCCCTTAATGTGGACTAAATAGGAGCTTGCGATTATTGATCT 104  
 QY 21 GlngLulgLylTrpLysLeuAlaValAlaLysLysProSerGlyAspAspArgTyr 40  
 Db 105 CAAGAGGGGAGGAGCTAGCTTAATTAACCACTGGATGATGATAC 164  
 QY 41 AspGln-PheHisIleArgArgPhenylalaleuIeuLysSerProThrSe 60  
 Db 165 AATCAAGTTTCACATAAGCATGGATTTGAACAT-CTTCAAATGGAAAAGTCACATTC 223  
 QY 60 rglLeuIeuPheAspTP-GlyThrIleAspCysThrValGlyAspLeuValAspLeu 80  
 Db 224 TTGATACCTGTTGACTCGGGGCCAACAAATGGAGCTTGATCTTGAGATCT 283  
 QY 80 euIleGluLysGluPheAlaProAlaSerIeuLeuIeuProAspAlaValPro 98  
 Db 284 TGATCCAAATGAAATT-TTGCTCTGCGAGCTTTCCTCCAGATCTGTRCC 338  
**RESULT 11**  
 US-09-966-451-10  
 ; Sequence 10, Application US/09966451  
 ; Publication No. US20030087856A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Susan M. Freier  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS  
 FILE REFERENCE: R7S-0324  
 CURRENT APPLICATION NUMBER: US/09/966,451  
 CURRENT FILING DATE: 2001-09-28  
 NUMBER OF SEQ ID NOS: 88  
 SEQ ID NO 10  
 LENGTH: 31000  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 US-09-966-451-10  
 Alignment Scores:  
 Pred. No.: 1.95e-27 Length: 31000  
 Score: 256.00 Matches: 49  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 98.00% Mismatches: 0  
 Query Match: 49.52% Deletions: 0  
 DB: Gaps: 0  
 RESULT 10  
 Sequence 149, Application US/09833790  
 Patent No. US2002006288A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lodes, Michael J.  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Sechrist, Heather  
 ; APPLICANT: Mohamath, Raodoh  
 ; APPLICANT: Indrias, Carol Y.  
 ; APPLICANT: Fan, Liqun

US-10-001-254-6 (1-98) x US-09-966-451-10 (1-31000)

QY 45 IleArgArgPheGlnAlaLeuLeuGlnThrGlySerProThrSerGluLeuPhe 64  
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 12963 TTAAGGAGATTTGAACTTCACACTGGAAAGTCCACTTGAACTTGAA 13022

QY 65 AspTrpGlyThrAsnCysThrValGlyAspLeuValAspLeuLeuGlnGlu 84  
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 13023 GACTGGCACACAAATTGCACAGTGTGATCTTGATCCAAATGAA 13032

QY 85 PhePheAlaProAlaSerLeuLeuLeuPro 94  
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 13083 TTTCGCTCTGGAGCTTGTCTCCA 13112

RESULT 12

US-10-630-399-10

; Sequence 10, Application US/10630399

; Publication No. US20040019009A1

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS FILE REFERENCE: RIS-US-024

CURRENT APPLICATION NUMBER: US/10/630,399

PRIOR FILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: US/09/966,451

PRIOR FILING DATE: 2001-09-28

NUMBER OF SEQ ID NOS: 88

SEQ ID NO 10

LENGTH: 31,000

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

; US-10-630-399-10

Alignment Scores:

Pred. No.: 1.95e-27

Score: 256.00

Percent Similarity: 100.00%

Best Local Similarity: 98.00%

Query Match: 49.52%

DB: 16

Length: 31000

Matches: 49

Conservative: 1

Mismatches: 0

Indels: 0

Gaps: 0

US-10-001-254-6 (1-98) x US-10-630-399-10 (1-31000)

QY 45 IleArgArgPheGluAlaLeuLeuGlnThrGlySerProThrSerGluLeuLeuPhe 64  
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 12963 TTAAGGAGATTTGAACTTCACACTGGAAAGTCCACTTGAACTTGAA 13022

QY 65 AspTrpGlyThrAsnCysThrValGlyAspLeuValAspLeuLeuGlnAsnGlu 84  
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 13023 GACTGGCACACAAATTGCACAGTGTGATCTTGATCCAAATGAA 13082

QY 85 PhePheAlaProAlaSerLeuLeuPro 94  
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 13083 TTTCGCTCTGGAGCTTGTCTCCA 13112

RESULT 13

US-10-001-254-25

; Sequence 25, Application US/10001254

; Publication No. US20030049702A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; APPLICANT: Godzik, Adam

; APPLICANT: Pawlowski, Krzysztof

; APPLICANT: Fiorentino, Noradina

; APPLICANT: Lee, Sung Hyung

; APPLICANT: Roth, Wilfred

; APPLICANT: Steiner-Liwen, Frank

; TITLE OF INVENTION No. US20030049702A1 el Death Domain Proteins

; FILE REFERENCE: P-LJ 5037

CURRENT APPLICATION NUMBER: US/10/001,254

RESULT 14

US-10-242-335A-26096

; Sequence 26096, Application US/10242535A

; Publication No. US20040013663A1

; GENERAL INFORMATION:

; APPLICANT: Chondrogenes Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4331/005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085, 783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305, 340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275, 017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271, 955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 26096

Length: 470

TYPE: DNA

ORGANISM: Human

US-10-242-535A-26096

Alignment Scores:

Pred. No.: 1.25e-28

Score: 241.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 47.78%

DB: 16

US-10-001-254-6 (1-98) x US-10-242-535A-26096 (1-470)

Qy 1 Thr<sup>Y</sup>ValArgCysLeuAlaValGlyLeuIleGlySerAspPheIleAspPro 20  
 Db 139 ACATATGTCGCCGCCTCAAGTGGACTTAATTAGGAAGCTGTAGATTATGATCT 198

Qy 21 GlngGluglyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40  
 Db 199 CAAGAGGATGAGAAGTAGTGCTGCTAGCTTAAACCATCTGGGAGTGTAGATAC 258

Qy 41 AsnGlnPheHisIleArg 46  
 Db 259 ATCAGTTTCACATAGA 276

RESULT 15  
 US-10-085-783A-26096  
 ; Sequence 26096, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Li,ew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 26096  
 ; LENGTH: 470  
 ; TYPE: DNA  
 ; - ORGANISM: Human  
 ; US-10-085-783A-26096

Alignment Scores:

Prod. No.:	Score:	Length:	MatcheB:	Conservative:	Mismatches:	Indels:	Gaps:
	1.25e-28	247.00	46	0	0	0	0
Percent Similarity:	100.00%	100.00%					
Best Local Similarity:							
Query Match:	47.78%						
DB:	16						

US-10-001-254-6 (1-98) x US-10-085-783A-26096 (1-470)

Qy 1 Thr<sup>Y</sup>ValArgCysLeuAlaValGlyLeuIleGlySerAspPheIleAspPro 20  
 Db 139 ACATATGTCGCCGCCTCAAGTGGACTTAATTAGGAAGCTGTAGATTATGATCT 198

Qy 21 GlngGluglyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40  
 Db 199 CAAGAGGATGAGAAGTAGTGCTGCTAGCTTAAACCATCTGGGAGTGTAGATAC 258

Qy 41 AsnGlnPheHisIleArg 46  
 Db 259 ATCAGTTTCACATAGA 276

Search completed: January 12, 2005, 09:54:48  
 Job time : 478 secs

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## us-10-001-254-6.p2n.rng

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: January 12, 2005, 05:39:30 ; Search time 412 Seconds  
 (without alignments)  
 1248.649 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517  
 Sequence: 1 TYVRCLNVGLRKLSDFIDP.....LLIQNEFFAPASLLIPDAVP 98

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

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-MODEL=frame+P2n.model -DEV=xlh
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-LOOPC1=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi
-LIST=15 -DOCALLIG=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL=LOCAL -OUTFILE=pto -INFILE=ext -HEAPSIZE=50000 -MINLEN=0 -MAXLEN=200000000
-USER=us10001254 @CGN 1_1 -470 @runat_10012005_172738_10451 -NCPU=6 -ICPU=3
-NOMMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCARPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : N\_Geneseq 23Sep04:\*

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

1	517	100.0	294	6	AD0074	Ad40074 Human IRA
2	517	100.0	294	6	AD09056	Adc59056 Human IRA
3	517	100.0	833	3	AA09319	AA09319 Human can
4	517	100.0	1383	6	AD40079	Ad40079 Human IRA
5	517	100.0	1383	6	AD59061	Ad59061 Human IRA
6	517	100.0	1668	5	AAS76805	Aas76805 DNA encod

7	517	100.0	2817	6	AAD40085	Ad40085 Human IRA
8	517	100.0	2817	6	AAD59067	Adc59067 Human IRA
9	517	100.0	2817	10	ACG47548	Acc47548 Human IL-
10	513	99.2	1383	5	AAD1017	Ad10197 Human int
11	476	92.1	1542	5	AAD10198	Ad10198 Mouse int
12	413	79.9	501	6	AAS81608	Aas81608 Lung small
13	256	49.5	405	5	AAS76803	Aas76803 DNA encod
14	256	49.5	31000	10	ACG47549	Acc47549 Human DNA
15	247	47.8	211	6	AAD40084	Ad40084 Human pro
16	247	47.8	211	6	AAD59066	Ad59066 Human IRA
17	247	47.8	415	5	AAST6802	Aas76802 DNA encod
18	247	47.8	2213	4	AAH13798	Ahh13798 Human cDN
19	247	47.8	2432	12	ADB28369	Ad28369 Human kpp
20	134.5	26.0	408	5	ABQ56733	Abq56733 Human col
21	18.7	18.7	1791	4	AAT44695	Aaf44695 Novel pro
22	96.5	18.7	1791	12	ADT29933	Adt2993 Human MAR
23	96.5	18.7	2277	4	AAC04459	Aac84459 Interleuk
24	96.5	18.7	2288	3	AAZ61602	Aaz61602 Human pol
25	96.5	18.7	2223	4	AAT157800	Aai57800 Human pol
26	96.5	18.7	2490	5	AAS86902	Aas86902 DNA encod
27	95	18.4	1888	9	ABD81345	Abd81345 cDNA encod
28	84	16.2	1494	5	AAS87194	Aas67194 DNA encod
29	79	15.3	1782	10	AD240440	Ade40440 Human IRA
30	79	15.3	1806	2	AAX77599	Aax77599 Human IRA
31	79	15.3	3459	2	AAX77600	Aax77600 Human IRA
32	78.5	15.2	861	4	AAL37224	Aal37224 Human mus
33	78.5	15.2	861	12	ADT30962	Adt30962 Human mus
34	78.5	15.2	861	12	ADT30962	Adt30962 Human mus
35	78.5	15.2	864	4	AAL37222	Aal37222 Human mus
36	78.5	15.2	864	4	AAL37225	Aal37225 Human mus
37	78.5	15.2	864	8	ABK60213	Abx60213 cDNA encod
38	78.5	15.2	864	8	ABK60210	Abx60210 cDNA encod
39	78.5	15.2	864	12	ADU30963	Adu30963 Human mus
40	78.5	15.2	864	12	ADU30960	Adu30960 Human mus
41	77	14.9	876	9	ABD7286	Adb7286 Murine My
42	75.5	14.6	3128	4	ADH02024	Adm02024 Human cDN
43	74.5	14.4	652	6	ABK53369	Abk53369 Human eos
44	74.5	14.4	774	6	ABK3720	Abk3720 Bacillus
45	72.5	14.0	2819	6	ABK52386	Abk52386 DNA encod

## ALIGNMENTS

RESULT 1	AD40074	ID AD40074 standard; cDNA; 294 BP.
XX	XX	XX
AC	AC	AD40074;
XX	XX	DT 22-OCT-2002 (first entry)
DE	Human	IRAK4 DD (death domain) cDNA.
XX	XX	Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ss.
XX	OS	Homo sapiens.
XX	KEY	Location/Qualifiers
FF	FT	1..294
FT	FT	/*tag= a /product= "Human IRA4 DD"
FT	FT	/note= "No start and stop codon"
FT	FT	/partial
FT	FT	Ad40074 Human IRA
FT	FT	Adc59056 Human IRA
FT	FT	AA09319 Human can
FT	FT	Ad40079 Human IRA
FT	FT	Ad59061 Human IRA
FT	FT	Aas76805 DNA encod

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PR	17-NOV-2000; 2000US-00715893.	QY	81 IleginangluPhephealaProAlaserleuleuProaspAlavalpro
PR	29-JUN-2001; 2001US-0301889P.	XX	98
PA	(BURN-) BURNHAM INST.	XX	294 ATCCAAATGATTTCGCTCCAGCTTGTGCTCC 294
XX		RESULT 2	
PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;	ID	AAD5056
PI	Stenner-Liewen F;	ID	AAD5056 standard; cDNA; 294 BP.
XX		XX	
DR	WPI: 2002-500222/53.	AC	AAD5056;
DR	P-FSDB; AAC24854.	AC	
XX		DT	18-DBC-2003 (first entry)
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.	XX	
PT	Claim 18; Page 173-174; 209pp; English.	XX	
XX	The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DRP3, IRAK4, CTD (Chlamydia trachomatis DD protein), DRP4 or NIDD (NCFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell, antibody specifically reactive with CTD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD cDNA.	XX	
CC	Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;	OS	Human IRAK4 DD cDNA.
CC	Alignment Scores:	XX	
CC	Pred. No.: 2.66e-64	FH	Human; death Domain; DD; death effector domain; DED; cell proliferation; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasoconstrictor; microbial infection; inflammation; allograft rejection; CTD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
CC	Score: 517.00	FT	KW
CC	Percent Similarity: 100.0%	FT	KW
CC	Best Local Similarity: 100.0%	FT	KW
CC	Query Match: 100.0%	FT	KW
DB:	Gaps: 0	FT	KW
US-10-001-254-6 (1-98) x AAD40074 (1-294)		XX	Homo sapiens.
QY	1 ThRTYvalArgCysLeuAsnValGlyLeuIleArglysLeuSerAspHeileAspPro	KEY	location/Qualifiers
QY	1 AGCTAATGTCGGCTGCCTCAATGTTGACTTAATGAGCTGTCAGTTTGACCT	1. .294	
QY	21 GingGlyLysTyrLysLeuIvalAlaLysLysProSerGlyAspAspTyr 40	/*tag= a	
QY	61 CAAGAAAGGATGAGAAGTGTAGCTTAAACCATCTGGTGATGATGATAC 120	/product= "Human IRAK4 DD protein"	
QY	41 AsnGlnPheHisIleGargArgPheGluAlaLeuIleGlnThrGlyLysSerProThrSer 60	/note= "No start and stop codon"	
QY	121 AACTAGCTTCACATAAGGAGTTGACCTACTCAACTGAGAAAGTCATCT 180		
QY	61 GluLeuIleAspProGlyLysIleAsnCysThrValGlyAspLeuAspLeu 80		
QY	181 GAACTGCTGTTGACTGGGGACCAATGCACTGACAGTGGGATCTTTG 240		
XX		PD	13-MAR-2003.
XX		PP	15-NOV-2001; 2001US-00001254.
XX		XX	PR 17-NOV-2000; 2000US-00715893.
XX		PR	17-NOV-2000; 2000US-0367360P.
XX		PR	29-JUN-2001; 2001US-0301889P.
XX		PA	(REED/) REED J C.
XX		PA	(GODZ/) GODZIK A.
XX		PA	(PAWL/) PAWLOWSKI K.
XX		PA	(FIOR/) FIorentino L.
XX		PA	(LEES/) LEE S H.
XX		PA	(ROTH/) ROTH W.
XX		PA	(STEN/). STENNER-LIEWEN F.
XX		PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
XX		PI	Stenner-Liewen F;
XX		DR	WPI; 2002-500222/53.
XX		DR	P-FSDB; AAC38897.
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.	XX	
PT	Claim 18; Page 33-34; 99pp; English.	XX	
CC	The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds DD, DED or NB-ARC domain from DRPs, IRAKs, CTD, DRP4 or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein	CC	

CC cell proliferation, cell stress responses, responses to microbial  
 CC infection and B cell immunoglobulin class switching. DBs, DBs and NB-ARC  
 CC domains and/or anti-DD, anti-DB or anti-NB-ARC domain antibodies are  
 useful for discovery of drugs that suppress infection, sepsis and other diseases.  
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.  
 CC DD, DB or NB-ARC domain proteins are used to treat infection, allergy,  
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte  
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,  
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries  
 following balloon angioplasty (restenosis). The invention is also used in  
 CC antibody therapy and gene therapy. The present sequence is human.  
 CC interleukin-1 receptor-associated kinase (IRAK)-4 DD cDNA  
 XX  
 SQ Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.66e-64 Length: 294  
 Score: 517.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-001-254-6 (1-98) x AAD59056 (1-294)  
 QY 1 Thr-Tyr-Val-Ala-Cys-Leu-Ala-Ser-Gly-Leu-Ile-Lys-Glu-Leu-Ser-Asp-Phenyl-Ala-Pro 20  
 DB 1 ACATATGTCGCCCTCAGTGTGGACTTATTTGGAAACGCTGTGATTTATGATCT 60  
 QY 21 Glu-Glu-Gly-Tyr-Ala-Phe-Ala-Val-Ala-Lys-Ser-Pro-Der-Gly-Yaspar-Arg-Tyr 40  
 DB 61 CAG-CAG-Agg-GAG-GAG-AAG-TAG-CAT-TAA-TAA-AAC-CAT-TGG-GAT-GAT-GAT-AC 120  
 QY 41 Asn-Gln-Phe-His-Ile-Gar-Gar-Glu-Ala-Leu-Leu-Gln-Thr-Gly-Lys-Ser-Pro-Thr-Ser 60  
 DB 121 AAC-TCA-GTT-TCA-CAT-TAG-GA-GAT-TGA-Ser-CAT-TAC-TCA-ACT-GAA-AAG-TCC-CACT-TCT 180  
 QY 61 Glu-Glu-Leu-Phe-Asp-Tyr-Gly-Thr-Thr-Ala-Ser-Cys-Thr-Val-Gly-Yaspar-Val-Ala-Phe-Leu 80  
 DB 181 GAAT-TAC-TGTT-GACT-GG-GC-CAC-CAC-ATG-CAC-GT-GAC-TCT-GAT-CCT-TTG 240  
 QY 81 Ile-Gln-Glu-Glu-Phe-His-Ila-Pro-Ala-Lys-Leu-Leu-Pro-Ser-Ala-Val-Pro 98  
 DB 241 ATCC-GAA-ATG-AAT-TG-TG-CT-GG-GA-GT-TTG-GT-CCT-CC-CAG-A-TG-C-T-CCC 294  
 RESULT 3  
 ID AAA09319  
 ID AAA09319 Standard: DNA; 833 BP.  
 AC AAA09319;  
 XX DT 10-AUG-2000 (first entry)  
 XX Human cancer associated antigen precursor DNA, clone NY-RBN-64.  
 XX KW renal cancer; cancer associated antigen precursor; diagnosis; cytostatic;  
 XX SS.  
 OS Homo sapiens.  
 XX FH Key  
 CDS 50. .670  
 FT /\*tag= a  
 PN WO200020587-A2.  
 XX PD 13-APR-2000.  
 XX FT CDS  
 XX DE Human IRAK4 gene #1.  
 XX AC ADD40079;  
 XX ID ADD40079 Standard: DNA; 1383 BP.  
 XX ADD40079;  
 XX DT 22-OCT-2002 (first entry)  
 XX DE Human IRAK4 gene #1.  
 XX KW Human; death domain; DD; death effector domain; DEB; Chlamydia infection;  
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;  
 KW immuno-suppressive; gene therapy; antisense therapy; gene; ds.  
 OS Homo sapiens.

PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX Obata Y, Gout I, Tureci O, Sahin U, Pfreundschuh M, Scanlan MJ;  
 PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A;  
 XX DR WPI; 2000-30374/26.  
 DR P-PSDB; AAY92347.  
 XX Preventing, diagnosing and/or treating disorders associated with abnormal  
 PT expression of human cancer associated antigens.  
 PT expression of human cancer associated antigens.  
 XX PS Claim 57; Page 85; 121pp; English.  
 XX AAA09310-20 are novel genes isolated by SREEX screening from a renal  
 CC cancer cell line 1973/10-4. The genes encode cancer associated antigen  
 CC precursors. These gene products are useful in methods for preventing,  
 CC diagnosing and/or treating disorders, especially cancer, associated with  
 CC abnormal expression of human cancer associated antigens. The method  
 CC comprises contacting a sample from a subject with an agent that  
 CC specifically binds to the nucleic acid molecule or expression product (or  
 CC fragment) complexed with a human leukocyte antigen (HLA) molecule and  
 CC determining the interaction between the agent and the nucleic acid  
 CC molecule or the expression product as a determination of the disorder  
 XX  
 SQ Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.14e-63 Length: 833  
 Score: 517.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-001-254-6 (1-98) x AAA09319 (1-833)  
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 DB 74 ACATATGTCGCCCTCAGTGTGGACTTATTTGGAAACGCTGTGATTTATGATCT 133  
 QY 21 Glu-Glu-Gly-Tyr-Ala-Phe-Ala-Val-Ala-Lys-Ser-Pro-Der-Gly-Yaspar-Arg-Tyr 40  
 DB 134 CAG-CAG-GTT-GAG-GAA-GCT-TG-TCT-TAA-TAA-AAC-CAT-TGG-GAT-GAT-GAT-AC 193  
 QY 41 Asn-Gln-Phe-His-Ile-Gar-Gar-Glu-Ala-Leu-Leu-Gln-Thr-Gly-Lys-Ser-Pro-Thr-Ser 60  
 DB 194 AAC-TCA-GTT-TCA-CAT-TAG-GA-GAT-TGA-Ser-CAT-TAC-TCA-ACT-GAA-AAG-TCC-CACT-TCT 253  
 QY 61 Glu-Glu-Leu-Phe-Asp-Tyr-Gly-Thr-Thr-Ala-Ser-Cys-Thr-Val-Gly-Yaspar-Val-Ala-Phe-Leu 80  
 DB 254 GAAT-TAC-TGTT-GACT-GG-GC-CAC-CAC-ATG-CAC-GT-GAC-TCT-GAT-CCT-TTG 313  
 QY 81 Ile-Gln-Glu-Glu-Phe-His-Ila-Pro-Ala-Lys-Leu-Leu-Pro-Ser-Ala-Val-Pro 98  
 DB 314 ATCC-GAA-ATG-AAT-TG-TG-CT-GG-GA-GT-TTG-GT-CCT-CC-CAG-A-TG-C-T-CCC 367  
 RESULT 4  
 ID ADD40079  
 ID ADD40079 Standard: DNA; 1383 BP.  
 XX ADD40079;  
 XX DE Human IRAK4 gene #1.  
 XX KW Human; death domain; DD; death effector domain; DEB; Chlamydia infection;  
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;  
 KW immuno-suppressive; gene therapy; antisense therapy; gene; ds.  
 OS Homo sapiens.

Key	Location/Qualifiers
PT	1. .1383
PT	/*tag= a
PT	/product= "Human IRAK4"
PN	WO200240680-A2.
XX	XX
PR	23-MAY-2002.
XX	XX
PR	15-NOV-2001; 2001WO-US014844.
XX	XX
PR	17-NOV-2000; 2000US-00715893.
PR	29-JUN-2001; 2001US-0301889P.
XX	XX
PA	(BURN-) BURNHAM INST.
PT	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PT	Stemmer-Liwen F;
XX	XX
DR	WPI; 2002-50022/53.
DR	P-PSDB; AAE24859.
XX	XX
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
PT	Claim 19; Page 180-182; 209pp; English.
CC	The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DEPD4 or NIDD (NCCR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectrometry (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 gene
CC	XX
CC	Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 other;
CC	XX
Alignment Scores:	
Pred. No.:	2.31e-63
Score:	517.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	6
Gaps:	0
Length:	1383
Matches:	98
Conservative:	0
Mismatches:	0
Indels:	0
Db	85 CAGAGGATSGAGAGTGTCTGCTACTTTAAACCATCTGGATGATAGATC 144
OY	41 AsnGlnpheHsIleArgLysLeuSerAspPheIleAspPro 20
Db	145 ARTCAAGTTCACTAGGAGTTGAGCTTACCTCAACTGGAAAGTCACCTCT 204
OY	61 GluLeuLeuPheAspPrglyThrThrAspCysThrValgLyserProThrSer 60
Db	205 GATTAATGTTGACTGGCCACCAATGCACTGAGCTTGAGCTCTGAGCTTGTG 264
OY	81 IleGlaAsnGluPheAlaProLaaLeuLeuLeuProPalaValPro 98
Db	265 ATCCAATGATTTTGCTCTCGAGATGCTGTTCC 318
RESULT 5	
ID	AAD59061
ID	AAD59061 standard; cDNA; 1383 BP.
XX	XX
AC	AAD59061;
XX	XX
DT	18-DEC-2003 (first entry)
DE	Human IRAK4 full length gene #1.
XX	XX
KW	Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasoconstrictor; microbial infection; inflammation; allograft rejection; CTDD; cell stress response; benign prostatic hyperplasia; antibiotic; NIPD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
KW	XX
KW	OS Homo sapiens.
XX	XX
PH	Key
CD	Location/Qualifiers
PT	1. .1383
PT	/*tag= a
PT	/product= "Human IRAK4 protein"
XX	XX
PN	US2003049702-A1.
XX	XX
PD	13-MAR-2003.
XX	XX
PR	15-NOV-2001; 2001US-00001254.
XX	XX
PR	17-NOV-2000; 2000US-00715893.
PR	29-JUN-2001; 2001US-0301889P.
XX	XX
(REED/)	REED J C.
PA	(GODZ/)
PA	Godzik A.
PA	(PAWL/)
PA	Pawlowski K.
PA	(FIOR/)
PA	Fiorentino L.
PA	(LEES/)
PA	Lee S H.
PA	(ROTH/)
PA	Roth W.
XX	XX
(STEN/)	STEMMER-LIWESEN F.
XX	XX
PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI	Stemmer-Liwen F;
XX	XX
DR	WPI; 2002-50022/53.
DR	P-PSDB; AAE38902.
XX	XX
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
PT	Claim 19; Fig 10A; 99pp; English.
CC	The present invention provides novel death domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also
CC	CC
CC	CC

CC provides death domain containing protein such as Chlamydia trachomatis  
 CC death domain containing protein (CtDD) DD and neural growth factor  
 CC receptor-interacting death domain (NIRD) DB. The invention is useful for  
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED  
 CC or NB-ARC domain from DAP3, IRAK4, CtDD, DED4 or NIRD with a candidate  
 CC binding agent and identifying an effective agent (e.g. protein or drug)  
 CC that modulates the association of a DD, DED or NB-ARC domain with protein  
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for  
 CC modulating the level of cell process such as apoptosis, cell adhesion,  
 CC cell proliferation, cell stress responses, responses to microbial  
 CC infection and B cell immunoglobulin class switching. DDS, DEBs and NB-ARC  
 CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are  
 CC useful for discovery of drugs that suppress infection, autoimmunity,  
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.  
 CC DDD, DED or NB-ARC domain proteins are used to treat infection, allergy,  
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte  
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,  
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries  
 CC following balloon angioplasty (restenosis). The present sequence is human  
 CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene  
 XX

Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.31e-63 Length: 1383  
 Score: 517.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AASD59061 (1-1383)

OY 1 ThryrValArgCysLeuasnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
 Db 25 ACATATGTCGCCCTCATGTTGACTTAATGAGCTTATGATCT 84  
 OY 21 GluGluGlyTrpIleLysLeuAlaValAlaLysLysProSerGlyAspPheArgTyr 40  
 Db 85 CAAGAAGGATGGAAAGTAGCTGTACATTAAACCACTGTGGATGATAGATAC 144  
 OY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlySerProThrSer 60  
 Db 145 ATCAGTTTCACATAGGAGATTGAGCTTCAACTGAAAGTCCACTCT 204  
 OY 61 GluLeuLeuPheAspPheGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
 Db 205 GAATGACTGTTGACTGGGCCACAAATGCAAGTGTGACTCTGATCTT 264  
 OY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98  
 Db 265 ATCCAAATGATTTTGCTCCAGATGCTGTTCC 318

RESULT 6  
 AAS76805  
 ID AAS76805 standard; cDNA; 1668 BP.  
 AC AAS76805;  
 XX  
 DT 13-FEB-2002 (first entry)  
 DB DNA encoding novel human diagnostic protein #12609.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-0054027.  
 XX  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HISB-) HISSEQ INC.  
 XX  
 PI Demanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 P-PDB; ABG12618.

PS Sequence 1668 BP; 571 A; 289 C; 332 G; 476 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.99e-63 Length: 1668  
 Score: 517.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-001-254-6 (1-98) x AAS76805 (1-1668)

OY 1 ThryrValArgCysLeuasnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
 Db 25 ACATATGTCGCCCTCATGTTGACTTAATGAGCTTATGATCT 84  
 OY 21 GluGluGlyTrpIleLysLeuAlaValAlaLysLysProSerGlyAspPheArgTyr 40  
 Db 85 CAAGAAGGATGGAAAGTAGCTGTACATTAAACCACTGTGGATGATAGATAC 144  
 OY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlySerProThrSer 60  
 Db 145 ATCAGTTTCACATAGGAGATTGAGCTTCAACTGAAAGTCCACTCT 204  
 OY 61 GluLeuLeuPheAspPheGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80  
 Db 205 GAATGACTGTTGACTGGGCCACAAATGCAAGTGTGACTCTGATCTT 264  
 OY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98  
 Db 265 ATCCAAATGATTTTGCTCCAGATGCTGTTCC 318



PA (ROTH/) ROTH W.  
 PA (STENNER/) STENNER-LIEWEN F.  
 XX  
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
 PI Stenner-Liewen F;  
 XX DR WPI; 2002-500222/53.  
 DR P-PSDB; AAE38908.

XX PT New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX PS Claim 18; Page 51-53; 99pp; English.

XX CC The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DEPD, NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DBs, DBDs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases.

CC DB, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte, hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 full length gene

XX SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.22e-63 Length: 2817  
 Score: 517.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indexes: 0  
 DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AACD59067 (1-2817)

Qy 1 ThryrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
 Db 74 ACATAGTGTGGCTGCCTCAATGTCAGTAACTTGAACCTGCTGAGTTATGATCT 133  
 134 CAAGAGGATCGAGAAGTGTGCTGAGTTGATGATA  
 Qy 21 GlngGlugIlyTrpLysLysLeuAlaValAlaLeuIleLysLysProSerGlyAspAspArgTyr 40  
 Db 134 CAAGAGGATCGAGAAGTGTGCTGAGTTGATGATA  
 Qy 41 AspGlnPheIleIleArgArgPheGluAlaLeuIleGlnThrGlyLysSerProThrSer 60  
 Db 194 ATCAGTTGTCACATAGGAGATTGAGATTACTTCACACTGGAAAGTCCTACTCT 253  
 Qy 61 GluLeuLeuPheAspTrpGlyThrThrAspCysThrValGlyAspLeuAlaLeu 80  
 Db 254 GAATTAATGTTGACTGGACGCCAACATTGCAAGTGATGTTGAGCTTGAGCTTGTG 313  
 Qy 81 IlegInAsnGluPhePheAlaProAlaSerLeuIleLeuProAspAlaValPro 98  
 Db 314 ATCCAATGATGTTGCTCGAGTTGCTCCAGATGCTGTC 367  
 RESULT 9 ACC47548

---

ID ACC47548 Standard; DNA; 2817 BP.  
 XX ACC47548;  
 XX 11-JUL-2003 (first entry)  
 XX Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.  
 XX Antisense therapy; cytostatic; antimicrobial; antiinflammatory;  
 XX interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;  
 XX inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;  
 XX gene; db.  
 XX OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 50. -1432  
 FT /tag= a  
 FT product= "IL-1 receptor-associated kinase-4"  
 XX WO2003028636-A2.  
 XX 10-APR-2003.  
 XX 26-SEP-2002; 2002WO-US030574.  
 XX 28-SEP-2001; 2001US-00966451.  
 XX PA (ISIS) ISIS PHARM INC.  
 XX Bennett FC, Freier SM;  
 XX WPI; 2003-363256/34.  
 DR P-PSDB; ABR4401.

XX PT New antisense oligonucleotides for modulating IL-1 receptor-associated kinase-4 gene expression, particularly useful for preventing, delaying or treating e.g. cancer (e.g. renal cancer), inflammatory disease or an infection.

XX PS Example 13; Page 80-83; 119pp; English.

XX The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridizing with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridizing with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding IL-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The antisense compounds are useful for diagnostics, therapeutics, prophylaxis, or as research reagents or kits. The current sequence represents the human IL-1 receptor-associated kinase-4 encoding sequence (GenBank accession number NM\_016123).

XX SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.22e-63 Length: 2817  
 Score: 517.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indexes: 0  
 DB: 10 Gaps: 0

US-10-001-254-6 (1-98) x ACC47548 (1-2817)

Qy 1 ThryrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20  
 Db 74 ACATAGTGTGGCTGCCTCATGTGATTAATGAGCTGTCAGTTATGATCT 133

Db 134 CAGAGAAGCTGGAGAAAGTTAGCTGTTACATTAACCATCTGGATGATGATAC 193  
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),  
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or  
 CC allergic rhinitis); transplant rejection, autoimmune diseases (e.g.,  
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or  
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),  
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of  
 CC the central nervous system (e.g., neurodegenerative disease), CD14  
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,  
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic  
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and  
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,  
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of  
 CC IRAK-4 activity or expression are used to inhibit signal transduction  
 CC resulting from the activation of an interleukin-1 receptor (IL-1R) / Toll  
 CC receptor in a cell. They also inhibit the activation of a transcription  
 CC factor that activates NF kappaB in the cell. IRAK-4 is used to create a  
 CC nonhuman transgenic animal which is useful for testing the function of  
 CC IRAK-4 in vivo. Generate models for the study of inflammatory  
 CC disorders and conditions and for the development of potential treatments  
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences  
 CC are also used in gene therapy and in antisense therapy

XX SQ Sequence 1383 BP; 463 A; 244 C; 283 G; 393 T; 0 U; 0 Other;

XX Alignment Scores:  
 XX Preg. No.: 8.59E-63 Length: 1383  
 XX Score: 513.00 Matches: 97  
 XX Percent Similarity: 98.98% Conservative: 0  
 XX Best Local Similarity: 98.98% Mismatches: 1  
 XX Query Match: 99.23% Indexes: 0  
 XX DB: 5 Gaps: 0

XX US-10-001-254-6 (1-98) x AAD10197 (1-1383)

XX QY 1 THRYTValArgCysLeuAlaValGlyLeuIleArgLeuSerAspPheLeAspPro 20  
 XX DB 25 ACATATGCGCTGCCTCACTGTTGCAATTAGGAAGCTGTCAGATTATGACCT 84

XX QY 21 GingLgLyTPlslysLeuAlaValIleLyslsprosArglyAspAsparArgYr 40  
 XX DB 85 CAGAGAAGCTGGAGAGGTAGCTGTAGCTATTAAACCATCTGGATGATGATAC 144

XX QY 41 AspGlnPheHisIleArgA9GluAlaLeuIleArgLgLeuSerAspPheLeAspPro 20  
 XX DB 145 ATCACTTCACTAGGAGCTTGTAGT 204

XX QY 61 GluLeuLeuPheAspTgIThrThrAlaCysThrValGlyAspLeuAspLeu 80  
 XX DB 205 GAATTACTGTTGACTGGGCCACCAATTGCAAGCTGGATCTTGATGATTTG 264

XX QY 81 IleGlnArgGluPheLeaAlaProLeuLeuLeuProAspAlaValPro 98  
 XX DB 265 ATCCAATGAAATTGTCCTCGAGCTTGTGCCCAGATGTTGTC 318

XX RESULT 11  
 XX AAD10198  
 XX ID AAD10198 Standard; cDNA; 1542 BP.

XX AC AAD10198;  
 XX DT 24-SEP-2001 (first entry)  
 XX PT 24-SEP-2001 (first entry)  
 XX DB Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.  
 XX  
 XX QM Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;  
 XX IL; anti-bacterial, anti-inflammatory; ophthalmological; vasotrophic; OPD;  
 XX chronic obstructive pulmonary disease; neuroprotective; chronic cough;  
 XX adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;  
 XX interstitial lung disease; allergic rhinitis; transplant rejection;  
 XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;  
 XX multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;  
 XX cardiovascular disease; atherosclerosis; neurodegenerative disease;  
 XX sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;  
 XX pulmonary diseases and diseases of the airway (e.g., adult respiratory  
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),  
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or  
 CC allergic rhinitis); transplant rejection, autoimmune diseases (e.g.,  
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or  
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),  
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of  
 CC the central nervous system (e.g., neurodegenerative disease), CD14  
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,  
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic  
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and  
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,  
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of  
 CC IRAK-4 activity or expression are used to inhibit signal transduction  
 CC resulting from the activation of an interleukin-1 receptor (IL-1R) / Toll  
 CC receptor in a cell. They also inhibit the activation of a transcription  
 CC factor that activates NF kappaB in the cell. IRAK-4 is used to create a  
 CC nonhuman transgenic animal which is useful for testing the function of  
 CC IRAK-4 in vivo. Generate models for the study of inflammatory  
 CC disorders and conditions and for the development of potential treatments  
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences  
 CC are also used in gene therapy and in antisense therapy

XX PI Wesche H, Li S;  
 XX DR WPI; 2001-451860/48.  
 XX DR P-FSDB; AKE05398.  
 XX  
 XX PT Novel human interleukin-1 receptor associated kinase polypeptide, useful  
 XX for identifying modulators of the polypeptide for treating gout, asthma,  
 XX allergic rhinitis, multiple sclerosis and skin cancer.  
 XX  
 XX Claim 7; Fig 2; 89P; English.

CC The present sequence is a cDNA encoding human interleukin (IL)-1 receptor  
 CC associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and  
 CC other receptors and act to transduce signals originating from the  
 CC activated receptors ultimately leading to a variety of downstream  
 CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4  
 CC inhibitors are useful for treating inflammatory diseases such as  
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory

KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;  
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;  
 KW sarcoidosis; transgenic animal; ss.  
 XX  
 OS Mus sp.  
 XX  
 PH location/Qualifiers  
 FT CDS 1. .1542  
 FT /\*tag= a /products "Mouse IRAK-4"  
 FT  
 XX  
 PN WO200151641-A1.  
 XX  
 PA (TULA-) TULARIK INC.  
 XX  
 PT Wesche H, Li S;  
 XX  
 DR WPI; 2001-451860/48.  
 XX  
 PT Novel human interleukin-1 receptor associated kinase polypeptide, useful  
 PT for identifying modulators of the polypeptide for treating gout, asthma,  
 PT allergic rhinitis, multiple sclerosis and skin cancer.  
 XX  
 PS Claim 26; FIG 4; 89pp; English.  
 XX  
 CC The present sequence is a cDNA encoding mouse interleukin (IL)-1 receptor  
 CC associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and  
 CC other receptors and act to transduce signals originating from the  
 CC activated receptors, ultimately leading to a variety of downstream  
 CC effects such as nuclear factor (NF)- $\kappa$ B activation. The IRAK-4  
 CC inhibitors are useful for treating inflammatory diseases such as  
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory  
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD),  
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or  
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,  
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or  
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),  
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of  
 CC the central nervous system (e.g., neurodegenerative disease), CD14  
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,  
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic  
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and  
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,  
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of  
 CC IRAK-4 activity or expression are used to inhibit signal transduction  
 CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll  
 CC receptor in a cell. They also inhibit the activation of a transcription  
 CC factor that activates NF $\kappa$ B in the cell. IRAK-4 is used to create a  
 CC nonhuman transgenic animal which is useful for testing the function of  
 CC IRAK-4 in vivo, to generate models for the study of inflammatory  
 CC disorders and conditions and for the development of potential treatments  
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences  
 XX  
 SQ Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1. 938-57 Length: 1542  
 Score: 476.00 Matches: 89  
 Conservative: 5  
 Percent Similarity: 95.92% Conservative:  
 Best Local Similarity: 90.82% Mismatches: 4  
 Query Match: 92.07% Indels: 0  
 DB: 5 Gaps: 0  
 US-10-001-254-6 (1-98) x AAD10198 (1-1542)

QY 1 ThriThrValArgCysLeuIleAsnValGlyLeuIleArgLeuSerAspHeIleAspPro 20  
 QY |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 187 ACATACATACGGCAACTTATGCGGAATCTTAGGAAGCTGCGGATTATGATCT 246  
 QY 21 GluGluGlyTrpLysLysLeuAlaValAlaLeuLysProSerGlyAspAspArgTyr 40  
 Db 247 CAGAGGSGTGAGAAATTAGAGTAATCAGTCAGTAAAGCCGGGGAGGAGAAC 306  
 QY 41 AsnGlnPheHisIleArgArgpheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60  
 Db 307 ATCGATGTCATATAAGGAGATTCGAACCTACTTCGACGCCGAAAGGCCACCTG 366  
 QY 61 GluLeuLeuPheAspPheGlyThrAsnCysThrValGlyAspLeuValAspLeu 80  
 Db 367 GAATCTGCTTTGACTGGGACACGACTGCACAGTGGCAGCTTGATGCTACTG 426  
 QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuIleProLspAlaValPro 98  
 Db 427 GTCCGAGATGAGCTTGTccccccACTCTGCTGCGGATGCCGTCCC 480  
 DR RESULT 12  
 XX  
 ID AAS61608  
 ID AAS61608 standard; cDNA; 501 BP.  
 AC AAS61608;  
 XX  
 DT 29-JAN-2002 (first entry)  
 XX  
 DE Lung small cell carcinoma antigen, cDNA #149.  
 XX  
 KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;  
 KW lung cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177168-A2.  
 XX  
 PR 18-OCT-2001.  
 XX  
 PR 11-APR-2001; 2001WO-US011859.  
 XX  
 PR 11-APR-2000; 2000US-0196780P.  
 PR 21-JUN-2000; 2000US-0213361P.  
 PR 01-SEP-2000; 2000US-0229763P.  
 PR 05-SEP-2000; 2000US-0230623P.  
 PR 14-SEP-2000; 2000US-0232563P.  
 PR 19-DEC-2000; 2000US-0257030P.  
 PR 08-JAN-2001; 2001US-0260795P.  
 XX  
 PR (CORI-) CORIXA CORP.  
 XX  
 PI Lodes MJ, Wang T, Mohamath R, Indrias CY;  
 XX  
 DR WPI; 2002-010896/01.  
 XX  
 PT Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;  
 PT Lung tumor polynucleotide and polypeptides useful in therapy and  
 PT diagnosis of cancer especially lung cancer.  
 XX  
 PS Claim 1; Page 174; 295pp; English.  
 XX  
 CC The invention relates to novel isolated lung small cell cancer antigen  
 CC polynucleotides (I) and polypeptides (II) used in a method of detecting  
 CC cancer in a patient. The method is optionally performed by utilising  
 CC oligonucleotides (III), where the biological sample from the patient is  
 CC contacted with (III), detecting the amount of polynucleotide hybridised  
 CC to (III) in the sample and comparing the amount of polynucleotide to a  
 CC predetermined cut-off value and thereby determining cancer in a patient.  
 CC (I), (II) or antigen-presenting cells expressing (II) is useful for  
 CC stimulating and/or expanding T cells specific for a tumour protein. The  
 CC method comprises contacting T cell with one of the components under  
 CC conditions to permit the stimulation and/or expansion of the cells. A  
 CC composition comprising (I) is useful for stimulating an immune response  
 CC in a patient and for inhibiting the development of a cancer especially

CC lung cancer in a patient. An isolated T cell population is useful for  
 CC removing tumour cells from the biological sample and for inhibiting the  
 CC development of cancer in a patient. AS51460-AS61874 represent novel  
 CC human lung small cell cancer antigen coding sequences of the invention  
 XX SQ Sequence 501 BP; 165 A; 102 C; 97 G; 134 T; 0 U; 2 Other;  
 Alignment Scores:  
 Pred. No.: 4.01e-49 Length: 501  
 Score: 413.00 Matches: 93  
 Percent Similarity: 94.00% Conservative: 1  
 Best Local Similarity: 94.00% Mismatches: 4  
 Query Match: 79.88% Indels: 4  
 DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AAS61608 (1-501)

QY 1 ThrTyrValArgCysIeuAsnValGlyLeuIleArgIlysIeuSerAspPheIleAspPro 20  
 Db 45 ACATATGTGCCCTGCCTCAATTGGACTTAATTAGGAGCTTCAGAATTATGACCT 104  
 QY 21 GluGluGlyTrpIlysLysLeuAlaValAlaIleSlysProArgIysAspAspArgT 40  
 Db 105 CAAGAGGAGTAGGAAGAGTGACTGAGTCACTTAANAAACATCTGCTGATGATAC 164

QY 41 AsnGln-PheIleIargGnPheGluAlaLeuLeuGlnThrGlyYssPrThrSe 60  
 Db 165 ATCAAGTTTCACTAGAGGATTTGAGCAT-CTRCAACTGGAAAAGGCCACTC 223

QY 60 rGluLeuLeuPheAspTRP-GlyThrThrAlaCysThrValGlyAspLeuValAspLeu 80  
 Db 224 TTGAATACTGTTGACTGGGGCACCAAAATTGAGATGTGATCTTGATCTT 283

QY 80 euIleGlnAsnGluPhePheAlaProLaaSerLeuLeuLeuProAspAlaValPro 98  
 Db 284 TGATCCAAAGGATT-TTCTCTCCCGAACGCTTGTGCTCCAGTGCTTCCTCC 338

RESULT 13

AAS76803 ID AAS76803 standard; cDNA; 405 BP.

XX AC AAS76803; DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #12607.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. Homo Sapiens.

XX OS WO200173067-A2.

XX PD 11-OCT-2001.

XX PP 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-0054217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

XX PI Dmanac RT, Liu C, Tang YT;

XX DR MPI; 2001-639362/73.

DR P-PSDB; ABG12616.

XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX

PS Claim 1; SEQ ID NO 12607; 103BP; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (I), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of products dependent on DNA and amino acid sequences. AS64197-AA94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.96e-27 Length: 405  
 Score: 256.00 Matches: 49  
 Percent Similarity: 98.00% Conservative: 1  
 Best Local Similarity: 98.00% Mismatches: 0  
 Query Match: 49.52% Indels: 0  
 DB: 5 Gaps: 0

US-10-001-254-6 (1-98) x AAS76803 (1-405)

QY 45 IleArgArgPheGluAlaLeuLeuGlnThrGlyYssPrThrSerLeuLeuHe 64  
 Db 1114 TTAAGGGAGATTGAGCATTAATTGAAAGTGCCACTCTGATATTGTT 173

QY 65 AspPhePheThrThrAlaCysThrAlaGlyAspLeuValAspLeuLeuLeuGlnAspGlu 84

Db 174 GACTGGGACCAACAAATTGCAAGGTGGATCTTGTGGATCTTTGATCCAATGAA 233

QY 85 PhePheAlaProAlaSerLeuLeuLeuPro 94

Db 234 TTTCCTCCCGAGCTTGTGCTCC 263

RESULT 14

ACC47549 ID ACC47549 standard; DNA; 31000 BP.

XX AC ACC47549;

XX DT 11-JUL-2003 (first entry)

XX DE Human DNA complement sequence # SEQ ID 10.

XX KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis; db.

XX OS Homo sapiens.

XX PN WO2003028636-A2.

XX PD 10-APR-2003.

XX PP 26-SEP-2002; 2002WO-US030574.

XX PR 28-SEP-2001; 2001US-00966451.

XX



Thu Jan 13 09:24:13 2005

us-10-001-254-6.p2n.rng

Page 12

Db 145 ||||| AATCAGTTCACATTAGA 162

Search completed: January 12, 2005, 07:14:08  
Job time : 421 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: January 12, 2005, 06:22:23 ; Search time 2550 SecondB  
(without alignments)  
1400.429 Million cell updates/sec

Title: US-10-001-254-6  
Perfect score: 537

Sequence: I TYVRCVLNGLIRKLSDFFIDP.....LLIONEPFAPASLLLPDAVP 98

Scoring table: BLOSUM62  
Xgapop 10.0 , Ygapext 0.5  
Ygapop 10.0 , Fgapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
DelOp 6.0 , Delext 7.0

Searched:

32822875 seqs., 16219865908 residues  
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-Q / cgn01 USP0 spool.h/USP0\_0001254/runat\_10012005\_172739\_10471/app\_query.fasta\_1.263  
-DB=EST -QFMT=FastA -SFMT=P2N -RHEAPSZ=500 -MLINLEN=0 -MAXLEN=2000000000  
-USER=USP001254 @CGN\_1\_1\_3437 @runat\_10012005\_172739\_10471 -NCPU=6 -ICPH=3  
-NO\_MMAP -LARGE\_QUERY -NEG\_SCORES=0 -WAIT -DEBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSHDS=1 -XGAPOP=1 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_htc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gbs1:\*
- 9: gb\_gbs2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match Length	DB ID	Description
1	517	100.0	859	BG164491
2	511	98.8	821	CK459029
3	509	98.5	811	BG164491
4	495	95.7	402	BB42619
5	495	95.7	666	CN718062
6	485	93.8	719	BB696981
7	476	92.1	503	CA538859
8	476	92.1	598	BQ52228
9	476	92.1	610	BB660378

RESULT 1	BG164491	LOCUS	BG164491	859 pp mRNA linear EST 06-FEB-2001
DEFINITION	602342026F1 NIH_MGC_89	Homo sapiens	CDNA clone IMAGE:4452055', mRNA sequence.	
ACCESSION	BG164491	VERSION	BG164491.1	GI:12671194
KEYWORDS		SOURCE	EST:	
		ORGANISM	Homo sapiens (human)	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 859)	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.ncbi.nih.gov/
TITLE	Unpublished (1999)	JOURNAL	Contact: Robert Strausberg, Ph.D.	
COMMENT	Email: cgags@mail.nih.gov	Tissue Procurement:	ATCC	
CDNA Library Preparation:	Life Technologies, Inc.	DNA Sequencing by:	The I.M.A.G.E. Consortium (LILM)	
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILM at: http://image.llnl.gov	found through the I.M.A.G.E. Consortium/LILM at:		
FEATURES	High quality sequence stop: 634.	Plate:	LILM0240	row: d column: 08
Source	1. .859	/organism="Homo sapiens"	/mol_type="mRNA"	/db_xref="IMAGB:4452055"
				/clone="IMAGB:4452055"

/tissue type="hypernephroma, cell line"  
 /lab\_host="DH10B (Phage-resistant)"  
 /clone\_lib="NIH MGC 89"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

**ORIGIN**

	Alignment Scores:	Length:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
Pred. No.:	7.9e-60	859	51.70	100.0%	100.0%	Query Match:	4
		Matches:	98	Conservative:	0		
		Mismatches:	0		0		
		Indels:	0		0		
		Gaps:	0		0		

US-10-001-254-6 (1-98) x BG164491 (1-859)

	Alignment Scores:	Length:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
Qy	1 Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Lys Leu Ser Asp Phe Leu Asp Pro	20	51.10	100.0%	100.0%	Query Match:	118
Db	59 ACATATGCGCGCTCTCATGTTGACTATTAGGAACGTGAGTTATGGATCT	20					
Qy	21 GlngIuglyTrpLysLysLeuValAlaLeuLysLysProSerGlyAspArgTyr	40					
Db	119 CAGAAAGCAGGAGAAGTTAGCTTGATGATGATGATGATGATGATGATC	178					
Qy	41 AsnGlnPheHistIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer	60					
Db	179 AACATGCTTCATAGTAGGATGATGATGATGATGATGATGATGATGATC	238					
Qy	61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuLeu	80					
Db	239 GAACTACTGTTGACTGGGGCACACAAATTGCAAGCTTGATCTTGATGCTTG	298					
Qy	81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro	98					
Db	299 ATCCAAATGAAATTGCTCCCGAGTCTTGTCTCCAGATGCTGTCC	352					

RESULT 2

	DEFINITION	LOCUS	DEFINITION	LOCUS
DEFINITION	CK459029	CK459029	DEFINITION	CK459029
ACCESSION	CK459029	233479 MARC 4PIG	ACCESSION	233479 MARC 4PIG
VERSION	CK459029.1	Sub scrofa	VERSION	Sub scrofa
KEYWORDS		(pig)	KEYWORDS	
SOURCE			SOURCE	
ORGANISM			ORGANISM	
JOURNAL			JOURNAL	
COMMENT			COMMENT	

Contact: Smith TPI,  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single Pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified with  
 cross match v0.990329.  
 Plate\_TMW8032 row: K column: 23  
 Seq primer: GIAATGGACAGCACTTATGGG.  
 Location/Qualifiers

1. .821  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /db\_xref="IMAGE:1773160"  
 /tissue\_type="embryonal carcinoma"

**ORIGIN**

	Alignment Scores:	Length:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
Qy	1 Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Lys Leu Ser Asp Phe Leu Asp Pro	20	51.10	98.98%	97.96%	Query Match:	292
Db	233 ACATATGCGCTGCCTCATGTTGACTATTAGGAACGTGAGTTATGGATCT	20					
Qy	21 GlngIuglyTrpLysLysLeuValAlaLeuLysLysProSerGlyAspArgTyr	40					
Db	293 CAAAGAGGAGCAGAACAGTTAGCTGAGCTGATGATGATGATGATGATC	352					
Qy	41 AsnGlnPheHistIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer	60					
Db	353 AACAGCTTCAATTAGGAGATCGAACAAATTGCAAGCTTGATCTTGATGCTTG	412					
Qy	61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuLeu	80					
Db	413 GAACTACTGTTGACTGGGGCACACAAATTGCAAGCTTGATCTTGATGCTTG	472					
Qy	81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro	98					
Db	473 GTCCAAATGAGTCTTGTGCCCGAGTCTTGTCTTGTCTTGTCTTGTCTTGTCTC	526					

RESULT 3

	DEFINITION	LOCUS	DEFINITION	LOCUS
DEFINITION	BG616438	BG616438	DEFINITION	BG616438
ACCESSION	BG616438	602645772F1 NIH_MGC_61	ACCESSION	602645772F1 NIH_MGC_61
VERSION	BG616438.1	Homo sapiens	VERSION	Homo sapiens
KEYWORDS		mRNA Sequence.	KEYWORDS	
EST.			EST.	
SOURCE			SOURCE	
ORGANISM			ORGANISM	
JOURNAL			JOURNAL	
COMMENT			COMMENT	

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.  
 (bases 1 to 821)  
 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,  
 Nonnem, D.J., Wray, J.E. and Keele, J.W.  
 Porcine EST collection using a normalized library constructed from  
 embryos representing early developmental stages  
 Unpublished (2003)  
 Contact: Smith TPI,  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single Pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified with  
 cross match v0.990329.  
 Plate\_TMW8032 row: K column: 17  
 Seq primer: GIAATGGACAGCACTTATGGG.  
 Location/Qualifiers

1. .811  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /db\_xref="IMAGE:1773160"  
 /tissue\_type="embryonal carcinoma"/>  
 /tissue type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 4 PIG"  
 /note="Vector: pCMV-SPORT6; Site 1: EcoRI; Site 2: NotI;  
 Library made with combined RNA from day-10, Day-13,  
 day-15, day-25, and day-30 whole embryos."

/lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MCC\_61"  
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1:  
 SfiI (ggccgcgtcgcc); Site\_2: SfiI (ggccctatggcc);  
 double-stranded cDNA was prepared from cell line RNA. 5'  
 and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGCCATATTGCC-3', and 3' adaptor  
 sequence: 5'-ATCTAGAGCCGAGGCACATG-dT(30)BN-3'  
 (where B = A, C, G, or T). Average  
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 laboratories (Palo Alto, CA). Note: this is a NIH\_MCC  
 library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 9.03e-59 Length: 811  
 Score: 509.00 Matches: 97  
 percent Similarity: 98.98% Conservative: 0  
 Best Local Similarity: 98.98% Mismatches: 1  
 Query Match: 98.45% Indels: 0  
 DB: 4 Gaps: 0

## US-10-001-254-6 (1-98) x BG616438 (1-811)

QY 1 ThrTyValArgCysLeuasnvalgyleuilearglyleuSerAspPheileAspPro 20  
 Db 77 ACATATGTCGCGCTCATGGTCACTTAATTAGAAGCTGTGAGTTATGATCT 136

QY 21 GlngluglyTpplvlysleuvalavalallelyslsypresrglylaspaspargyr 40  
 137 CAAGAGGAGTAGGAAGATGTTAGCTTGACTTAATTAGAAGCTGTGAGTTATGATCT 196

QY 41 AsnGlnPhenHisileargargphegluvalleuileuglnthrGlyLysSerProThrSer 60

Db 197 ATcAGTTCACATAAGGAGTTGAACTTACTTCAACTGGAAAGTCCACTCT 256

QY 61 GlueuleLeupheAspTPrglyThrthrAsnCysThrValGlyAspLeuValAspLeu 80

Db 257 GAATACTGTTGACTGGGGCACACACAATTGCAAGTGTGGTGAATCTGATCTTG 316

QY 81 IlegInAsnGluPhePheAlaProLaaSerLeuLeuLeuProApAlaValPro 98

Db 317 ATCCAAATGATTCTGCTCTGAGCTTGTCTCCAGATGCTGTCTCCC 370

## RESULT 4

BE482619 LOCUS BB482619 402 bp mRNA linear EST 27-MAR-2003  
 DEFINITION 168463 BARC SBOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION BB482619  
 VERSION BE482619.1 GI:9620152

KEYWORDS EST, Bos taurus (cow)

SOURCE  
 ORGANISM Bos taurus  
 Bos tauru(Bovinae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovine)

REFERENCE 1. (bases 1 to 402)  
 AUTHORS Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Wells, K.D., Connor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.

TITLE Analysis of bovine mammary gland EST and functional annotation of Mamm. Genome 13 (7), 373-379 (2002)  
 MEDLINE 22135296  
 PUBMED 12140584  
 COMMENT Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414  
 Email: tadsolpsi.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.s. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCGCCACGTCACGAC  
 Plate: 11 row: F column: 7  
 Seq primer: ATTAGGAGCAGTATAG  
 1. -402  
 Location/Qualifiers  
 /mol type="mRNA"  
 /organism="Bos taurus"  
 /db\_xref="Taxon:9913"  
 /tissue\_type="pooled"  
 /clone\_lib="BARC SBOV"  
 /note="Vector: pcMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
 Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."  
 ORIGIN

## FEATURES source

Alignment Scores:  
 Pred. No.: 2.89e-57 Length: 402  
 Score: 495.00 Matches: 92  
 Percent Similarity: 97.96% Conservative: 4  
 Best Local Similarity: 93.88% Mismatches: 2  
 Query Match: 95.74% Indels: 0  
 DB: 2 Gaps: 0

## US-10-001-254-6 (1-98) x BE482619 (1-402)

QY 1 ThrTyValArgCysLeuasnvalgyleuilearglyleuSerAspPheileAspPro 20  
 Db 88 ACATATGTCGCGCTCATGGTCACTTAATTAGAAGCTGTGAGTTATGATCT 147

QY 21 GlngluglyTpplvlysleuvalavalallelyslsypresrglylaspaspargyr 40  
 148 CAAGAGGAGTAGGAAGATGTTAGCTGCGCTCATGGTCACTTAATTAGAAGCTGTGAGTTATGATCT 207

QY 41 AsnGlnPhenHisileargargphegluvalleuileuglnthrGlyLysSerProThrSer 60

Db 208 ATcAGTTCACATAAGGAGTTGAACTTACTTCAACTGGAAAGTCCACTCT 267

QY 61 GlueuleLeupheAspTPrglyThrthrAsnCysThrValGlyAspLeuValAspLeu 80

Db 268 GAATACTGTTGACTGGGGCACACACAATTGCAAGTGTGGTGAATCTGATCTTG 381

## RESULT 5 CN788062

LOCUS CN788062 666 bp mRNA linear EST 26-MAY-2004  
 DEFINITION 4122347 BARC 8BOV Bos taurus cDNA clone 8BOV\_26007 5', mRNA sequence.  
 ACCESSION CN788062  
 VERSION CN788062.1 GI:47684042

KEYWORDS EST, Bos taurus (cow)

SOURCE  
 ORGANISM Bos tauru(Bovinae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovine)

REFERENCE 1. (bases 1 to 666)  
 AUTHORS Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.  
 TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Richard G. Baumann  
 Bovine Functional Genomics Lab

		ANRI	BLOC 162: BARC-EAST, Beltsville, MD 20705, USA
Tel:	3015048604	REFERENCE	1 (bases 1 to 71)
Fax:	3015048744	AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
Email:	rbaumann@anri.barc.usda.gov	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
Single pass sequencing.		JOURNAL	Unpublished (1999)
0-000925 using options -trim_alt , -trim_fasta. Vector identified by cross match using options -mismatch 12 -minscore 18		COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgrabs@mail.nih.gov
Seq primer: CCTATTTAGGGACACTATAGAAC		Tissue Procurement: ATCC	
High quality sequence stop: 666.		cDNA Library Preparation: CLONETECH Laboratories, Inc.	
FEATURES	source	CDNA Library Arrived by: The I.M.A.G.E. Consortium (LNU)	
Location/Qualifiers		DNA Sequencing by: Incyte Genomics, Inc.	
1. .666		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLU at:	
/organism="Bos taurus"		http://image.lnl.gov	
/mol_type="mRNA"		Plate: LNCM124 Row: 9 Column: 15	
/strain="Holstein"		High quality sequence stop: 632.	
/db_xref="taxon:9913"		Location/Qualifiers	
/clone="8BOV_26007"		1. .713	
/sex="female"		/organism="Homo sapiens"	
/tissue_type="Epithelial, Muscle"		/mol_type="mRNA"	
/dev_stage="Lactating, Neonatal"		/db_xref="taxon:9606"	
/lab_host="DH10B Tona"		/clone="IMAGE:4287014"	
/clone_lib="BARC 8BOV"		/tissue_type="primitive neuroectoderm"	
/note="Organ: Intestine; Vector: pcMVSPORT6.1; Site_1: NTII; Site_2: EC86; Normalized cow cDNA intestinal library in pcMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal, 4/5 Lactating, Proximal Duodenum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"		/lab_host="DH10B (T1 phage-resistant)"	
Query Match: 95.74%	7	/clone_lib="NIH_MGC_56"	
DB:	Gaps:	/note="Organ: brain; Vector: pDMR-LIB (Clontech); Site_1: SfI (ggccgcctggcc); Site_2: SfiI (ggccattaggcc); Double stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5', adaptor sequence: 5'-ATTCGAGCCGGCGGCCGACATGAT(30)BN-3, (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."	
US-10-001-254-6 (1-98) x CN788062 (1-666)		Alignment Scores:	
Pred. No.:	5.74e-57	Length:	666
Score:	495.00	Matches:	92
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Best Local Similarity:	93.88%	Mismatches:	2
Query Match:	95.74%	Indels:	0
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
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DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
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DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
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Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
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Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
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DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
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DB:	Gaps:	ORIGIN	
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Score:	485.00	Matches:	97
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DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
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DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
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Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
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Best Local Similarity:	97.00%	Mismatches:	1
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DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%	Mismatches:	1
Query Match:	93.81%	Indels:	2
DB:	Gaps:	ORIGIN	
US-10-001-254-6 (1-98) x BR696981 (1-719)		Alignment Scores:	
Pred. No.:	1.49e-55	Length:	719
Score:	485.00	Matches:	97
Percent Similarity:	97.00%	Conservative:	0
Best Local Similarity:	97.00%</td		



Query Match:		92.07%	Indels:	0
		5	Gaps:	
QY	1 ThrThrValArgCysLeuAsnValGlyLeuIleArgCysLeuSerAspPheIleAspPro	20		
Db	176 ACATCATACGAACTTAATGCGGATCTTGGAGCTTATTGATCT 235			
QY	21 GluGluGlyTrpPheIleAsnValGlyLeuIleArgCysLeuSerAspPheIleAspPro	20		
Db	236 CAAGAGGGTGAACTTAATGCGGATCTTGGAGCTTATTGATCT 295			
QY	41 AspGlnPheIleAsnGlyPheGluAlaLeuIleGlnThrGlyLysSerProThrSer	60		
Db	296 AACATGGTCCTCCATATAAGGAACTTCAAGCTTAATGCGGATCTTGGAGCTTATTGATCT 355			
QY	61 GluLeuLeuPheAspPheIleAsnValGlyAspLeuValAspLeu	80		
Db	356 GACTGCCTTTGACTGGGCCACCGAACATGCGATGTCAGTGGACGATCTG 415			
QY	81 IleGlnAsnGluPheIleAlaProAlaSerLeuLeuProAspAlaValPro	98		
Db	416 GTCCAGATTGAGCTTTGCCCTCCACTCTCTGCGGATGCCGTTC 469			
RESULT 9				
LOCUS	BB660378			
DEFINITION	BB660378 RIKEN full-length enriched, 13 days embryo EST 26-OCT-2001	610 bp mRNA linear EST 26-OCT-2001		
MATERIALS	musculus cDNA clone D430042L21 5', mRNA sequence.			
VERSION	BB660378.1			
EST.	GI:16494199			
KEYWORDS				
SOURCE				
ORGANISM	Mus musculus (house mouse)			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; sciurognath; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 610)			
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Murayama,T., Mizazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Soejima,Y., Suzuki,H., Tagami,M., Togawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.			
JOURNAL	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
COMMENT	Contact: Yoshinide Hayashizaki, Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Unpublished (2001)			
TITLE				
JOURNAL				
COMMENT				
ORIGIN				
Alignment Scores:				
Pred. No.:	2.03e-54	Length:	610	
Score:	476.00	Matches:	89	
Percent Similarity:	95.92%	Conservative:	5	
Best Local Similarity:	90.82%	Mismatches:	4	
Query Match:	92.07%	Indels:	0	
DB:	2	Gaps:	0	
US-10-001-254-6 (1-98) x BB660378 (1-610)				
QY	1 ThrThrValArgCysLeuAsnValGlyLeuIleArgCysLeuSerAspPheIleAspPro	20		
Db	212 ACATCATACGAACTTAATGCGGATCTTGGAGCTTATTGATCT 271			
QY	21 GluGluGlyTrpPheIleAsnValGlyLeuIleArgCysLeuSerAspPheIleAspPro	20		
Db	272 CAAGAGGGTGAACTTAATGCGGATCTTGGAGCTTATTGATCT 331			
QY	41 AspGlnPheIleAsnGlyPheGluAlaLeuIleGlnThrGlyLysSerProThrSer	60		
Db	332 ATCAGTTCCATATAAGGAGATGCGGATCTTGGAGCTTATTGATCT 391			
QY	61 GluLeuLeuPheAspPheIleAsnValGlyAspLeuValAspLeu	80		
Db	392 GACTGCCTTTGACTGGGCCACCGAACATGCGATGTCAGTGGACGCTTATTGATCTG 451			
QY	81 IleGlnAsnGluPheIleAlaProAlaSerLeuLeuProAspAlaValPro	98		
Db	452 GTCCAGATTGAGCTTTGCCCTCCACTCTGCGGATGCCGTTC 505			
RESULT 10				
LOCUS	BB613447			
DEFINITION	BB613447 RIKEN full-length enriched, 10 day neonate skin Mus	637 bp mRNA linear EST 26-OCT-2001		
MATERIALS	musculus cDNA clone 473248P03 5', mRNA sequence.			
VERSION	BB613447			
EST.	GI:16454055			

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
REFERENCE	1 (bases 1 to 637)
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Mizazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sami,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tadawa,A., Takahashi,F., Takeeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Chemical and Institute of Physical and Chemical Research (RIKEN) 1-7-22, Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-5222 Fax: 81-45-503-5216 Email: genome-rs@gc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci,P., Shibata,K., Hayatsu,N., Suganara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Res.</i> . 10 (10), 1617-1630 (2000)
wagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Irawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsurua,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	
RIKEN integrated Sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicillary sequencer. <i>Genome Res.</i> . 10 (11), 157-171 (2000)	
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.	
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. <i>Genome Res.</i> . 11 (2), 281-289 (2001)	
Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamamoto,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.	
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. <i>Mamm. Genome</i> . 12, 673-677 (2001)	
Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details.	
FEATURES	e mouse tissues.
source	Location,Qualifiers
1. . 637 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:0090" /clone="473482P03" /sex="mixed" /tissue_type="skin" /dev_stage="10 days neonate" /lab_host="NH10B" /clone_lib="RIKEN full-length enriched, 10 day neonate" /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGATTCCTCGAGTTAAATAATCCCCCCCCCC 3']. cDNA was cloned into the XbaI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"	

SOURCE	sequence [5' GAGAGAGAGATTCCTCGAGTTAAATAATCCCCCCCCCC 3']. cDNA was cloned into the XbaI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
ORGIN	
Alignment Scores:	
Pred. No.: 2.15e-54	Length: 637
Score: 476.00	Matches: 89
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Best Local Similarity: 90.82%	Mismatches: 4
Query Match: 92.07%	Indels: 0
DB: 2	Gaps: 0
US-10-001-254-6 (1-98) x BB613447 (1-637)	
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Db	193 ACATCATACAGCACTTAATGAGGGCTCTTGGAGCTGAGGATTGATCT 252
QY	21 GlngIuglyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db	253 CAAGAGGGAGAATTAGCAGTAGCTATCAAACCCGGTCCGGCGACGAGATAC 312
QY	41 AsngInPhisIleArggPheGluLaleLeuLugInThrGlyLysSerProThr 60
Db	313 AATCAGTCATATTAGGAGATTCGAACTCTACTTCGACCCGGAAAGCCCACTCT 372
QY	61 GluIfeulePheAspTrpGlyThrThrAcnySthrValGlyAspLeuValProLeu 80
Db	373 GAACGCTGTTGACTGCGGCCACGACTGCGAGTTGGGACCTTGCTGTCGGATGCCCCTTCC 486
QY	81 IlegInAsglLugLphePheAlaProLaseLeuLeuLuproAspAlaValPro 98
Db	433 GTCCAGATGCTGTTGCGGCCACTCTCTGCTGTCGGATGCCCCTTCC 486
RESULT 11	
BY721552	
LOCUS	BY721552
DEFINITION	BY721552 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330209D03 5', mRNA sequence.
ACCESSION	BY721552
VERSION	BY721552.1 GI:27134669
KEYWORDS	EST.
SOURCE	
ORGANISM	Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
REFERENCE	1 (bases 1 to 638)
AUTHORS	Okazaki,Y., Furuno,M., Kawakawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamamoto,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Haegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baodarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schmidl,L.M., Kanapin,A., Matsuda,H., Batalov,S., Besel,K.W., Blake,J.A., Bridt,D., Brusic,V., Chothia,C., Corbin,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frerz,K.S., Gaasterland,T., Giaboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawabata,Y., Kedzierski,R.M., King,B.L., Konig,A., Kurachkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltsev,L., Marchionni,L., McKenzie,I., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavon,W.J., Pettea,G., Pesole,G., Petrovsky,N., Pilai,R., Pontius,J.U., Qi,D., Ramchandran,S., Ravasi,T., Reed,J.D., Reid,J., Ring,B.Z., Ringdahl,M., Sandelin,A., Schneider,C., Seiple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Terasdale,R.D., Tonita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Wakabayashi,Y., Wells,C., Wilming,L.G., Wynnshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishino,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Itohi,Y.,





FEATURES	DEFINITION
source	Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamamoto, I., Aizawa, K., Fukuda, S., Hara, A., Itou, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
	Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details.
Location/Qualifier	e mouse tissues.
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/dev_stage="10 days neonate"	
/lab_host="DH10B"	
/clone_lib="RIKEN full-length enriched, 10 day neonate skin"	
/note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCAAGCTTCTTTTTTTTWTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCCGAGTAATTAATGCCCGCCCCCCC 3']. cDNA was cloned into the XbaI and BamHI sites vector; a modified pBluescript KS(+) after bulk excision from Lambda FLC I"	
ORIGIN	
Alignment Scores:	
Scored. No.: 2.34e-54	Length: 676
Score: 476.00	Matches: 89
Percent Similarity: 95.92%	Conservative: 5
Best Local Similarity: 90.82%	Mismatches: 4
Query Match: 2	Indels: 0
DB: Gaps: 0	
US-10-001-254-6 (1-98) x BB613167 (1-676)	
REFERENCE	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Europ. J. Biochem. 253, 19-44 (1999)
MEDLINE	99279253
PUBMED	103149636
REFERENCE	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sakai, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kutsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hacama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikeda, T., Kashiwagi, K., Fujikake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer
TITLE	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	2053013
PUBMED	11076861
REFERENCE	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haanagi, T., Hara, A., Hayatsu, N., Hiramoto, H., Itoh, M., Hirao, T., Imamura, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurimaru, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Oya, C., Saito, H., Saio, R., Sakai, C., Sakai, K., Sanjo, H., Sasaki, D., Shibata, K., Sribata, K., Shingawa, A., Shiraki, T., Sobage, Y., Suzuki, H., Tagami, M., Tagawa, A., Tamaki, F., Tanaka, T., Teijima, Y., Tora, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshihiko, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-rep@gsc.riken.jp), URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> , Tel: 81-45-503-9222, Fax: 81-45-503-9216	
COMMENT	On Oct 4, 2001 this sequence version replaced gi:12866970. Please visit our web site ( <a href="http://genome.replace.gsc.riken.jp/">http://genome.replace.gsc.riken.jp/</a> ) for further details.
CDSNA library was prepared and sequenced in Mouse Genome Project (GSC).	
RESULTS	14
AK020397	1161 bp mRNA linear RT-PCR 03-APR-2004
AK020397	1161 bp mRNA linear RT-PCR 03-APR-2004

	Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken.
	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15', GAGAGAGAGGAGGACCAAGAGCTTCTTTTNTTN 3', cDNA was prepared by using trichloroacetic acid (TCA) and subsequently enriched for full-length by cap-trapper. cDNA went through two rounds of normalization to Rot = 20.0 and subtraction to Rot = 370.4. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATTCGAGTAACTTAATTAATCCCCCCCC 3']. cDNA was cleaved with BamHI and KhoI. Vector: a modified pBlue-script KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3', end: BamHI. Host: DH50B.
FEATURES	Location Qualifiers
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ORIGIN	
Alignment Scores:	
Pred. No.:	4.888-54
Score:	476.00
Percent Similarity:	95.92%
Best Local Similarity:	9.02%
Query Match:	92.07%
DB:	3
US-10-001-254-6 (1-98) x AK020397 (1-1161)	
QY	1 Thr>Val>Arg>Cys>Leu>Ala>Val>Gly>Leu>Ile>Arg>Gly>Leu>Ser>Asp>Phe>Leu>Asp>
Db	2 07 ACATACATACGCAACCTTAATGCTGGGACGCTGGATTATGATCTT 265
QY	21 GlngGlglVlPrlyBls>Leu>Ala>Val>Ile>Bls>Leu>Pro>Ser>Arg>Gly>Asp>Arg>Tr 40
Db	267 CAAAGAGGGGTGGAGAATGAGCTAGTCTCATCAAAGGCCGTCGGCAGACAGATC 326
Qy	41 Asp>Gln>Phs>Ile>Arg>Arg>Phe>Glu>Ala>Leu>Leu>Ile>Gly>Ser>Pro>Thr>Ser 60
Db	327 ATCAGTTCATATAGGAGATCGAACGTTACAGCCGAGGAGCCCCACCTT 386
QY	61 Glue>Leu>Phe>Asp>Trp>Gly>Thr>Thr>Asp>Cys>Thr>Val>Gly>Asp>Leu>Val>Asp>Leu 80
Db	387 GAACATGCTCTTGACTGGGACCCAGCAACTGCACTGAGCTTGAGCTACTG 446
QY	81 1le>Gln>Asp>Glu>Phe>HeLa>Pro>Ala>Ser>Leu>Leu>Pro>Asp>Ala>Val>Pro 98
Db	447 GTCCGAGATGAGCTGTTGCCGCCACTCTCCCTGCTGCCGATGCCGTTCC 500
RESULT 15	AK028837 AK028837 2481 bp mRNA linear HTC 03-APR-2004
LOCUS	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DEFINITION	
library, clone:4732460109 product:interleukin-1 receptor-associated kinase 4 [Mus musculus], full insert sequence.	
	ACCESSION AK028837
	VERSION 1
	KEYWORDS GL:26324783
	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	9927953
PUBMED	10349636
REFERENCE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Akiyama,J., Nishi,M., Tashiro,H., Ichio,M., Sumi,N., Ichihi,Y., Nakamura,S., Hazama,M., Nishime,T., Harada,T., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsubara,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis system (RISE) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (10), 1757-1771 (2000)
JOURNAL	2053013
PUBMED	11076613
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
AUTHORS	5
REFERENCE	The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL	6 (bases 1 to 2481)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagata,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirao,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Mizraiki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohshiro,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shiba,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tegawa,A., Takahashi,F., Takaku-Akabira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
REFERENCE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-researc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

## Location/Qualifiers

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/dev\_stage="10 days neonate"  
116\_1495  
CDS

ג'תנו

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Query Match:	90.82%	Indels:	0
DB:	92.07%	Gaps:	0
us-10-001-254-6 (1-98) x AK028837 (1-2481)			
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Db	140 ACAAATACATACCGAACCTTAATGTGGCGATCCATTAGCGTCCGATTTATTCCT	199	
Qy	21 GInGluGlyTrpLysIleuAlaValAlaLeuLysLysProSerGlyAspAspArgTyr	40	
Db	200 CAAGAAGGCTGGAAGAAATAGCAGCTAGCTATCACAAAAGCGTCGCCGAGCAAGATAC	259	
Qy	41 AsnGlnPheHistIleArgArgPheGluAlaLeuIleGlnThrGlyLysSerProThrSer	60	
Db	260 AATCAGTTCATATAAGGAGATCCAGGCCTACTTGAGACGGAAAGCCCCACCTGT	319	
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Qy	81 IleGlnAsnGluPhePheAlaProLaserLeuIleLeuProAspAlaValPro	98	
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Job time : 2555 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: January 12, 2005, 06:32:57 ; Search time 88 Seconds  
 791,560 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517

Sequence: TYVRCVLNLGILRKLSDFIDP.....LLIQNEFFAPASLLLPDAVP 98

Scoring table: BLOSUM62

xgapop 10.0 , xgapext 0.5  
 ygapop 10.0 , ygapext 0.5  
 fgapop 6.0 , fgapext 7.0  
 delop 6.0 , delext 7.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/usptp/spool/h/us0001254/runat10012005_172739_10481/app/query.fasta_1.263
-DB=US-PATENTS_NA -QFORMAT=fastap -SUFFIX_P2N.rni -MINMATCH=0.1 -DOOPCI=0
-LOOPEXT=0 -UNITS=5its -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=5000 -MINLEN=0 -MAXLEN=200000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADD=1 -XGAPOP=0 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPO=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	517	100.0	833	US-09-166-350-10 Sequence 10, Appli
2	517	100.0	2817	Sequence 4, US-09-966-451-3 Sequence 3, Appli
3	256	49.5	31000	Sequence 4, US-09-966-451-10 Sequence 10, Appli
4	96.5	18.7	2288	Sequence 3, US-09-135-232-1 Sequence 1, Appli
5	96.5	18.7	2288	Sequence 4, US-09-863-549-4 Sequence 1, Appli
6	79	15.3	1806	Sequence 2, US-08-980-060-1 Sequence 1, Appli
7	79	15.3	1806	Sequence 3, US-09-307-185-1 Sequence 1, Appli
8	79	15.3	3459	Sequence 2, US-08-980-060-3 Sequence 3, Appli
9	79	15.3	3459	Sequence 3, US-09-307-185-3 Sequence 3, Appli
10	79	15.3	3459	Sequence 4, US-09-773-753-3 Sequence 3, Appli
11	79	15.3	3459	Sequence 4, US-09-773-753-3 Sequence 3, Appli
c 12	78.5	15.2	479	US-10-001-254-6 (1-98) x US-09-166-350-10 (1-833) Sequence 14, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-166-350-10

; Sequence 10, Application US/09166350A

; Patent No. 6440633

; GENERAL INFORMATION:

; APPLICANT: Scanlan, Matthew

; APPLICANT: Chen, Yao

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Old, Lloyd

; APPLICANT: Jager, Elke

; APPLICANT: Knuth, Alex

; TITLE OF INVENTION: Renal Cancer Associated Antigens and

; TITLE OF INVENTION: Uses Therefor

; FILE REFERENCE: L0461/7051

; CURRENT APPLICATION NUMBER: US/09/166,350A

; CURRENT FILING DATE: 1998-10-05

; EARLIER APPLICATION NUMBER: US 09/166,350

; EARLIER FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO: 10

; LENGTH: 833

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-166-350-10

; Alignment Scores:

; Pred. No.: 3.96e-72

; Score: 517.00

; Percent Similarity: 100.00%

; Best Local Similarity: 100.00%

; Query Match: Gaps: 0

Sequence 14, Appli	Sequence 14, Appli
Sequence 1, Appli	Sequence 1, Appli
Sequence 2, Appli	Sequence 2, Appli
Sequence 3, Appli	Sequence 3, Appli
Sequence 4, Appli	Sequence 4, Appli
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Sequence 98, Appli	Sequence 98, Appli
Sequence 99, Appli	Sequence 99, Appli
Sequence 100, Appli	Sequence 100, Appli

QY 1 ThrtyValArgCysLeuIvaLvaValGlyLeuIleArglyLeuSerAspPheIleAspPro 20 ; Sequence 10, Application US/09966451  
Db 74 ACATATGTCGCTGCCTCAATGTCAGTGTGACTTTAGAGCTTGTCAGATTATGATCT 133 ; patent No. 6693959  
; GENERAL INFORMATION:  
QY 21 GlnglGluGlyTrpLySlysLeuIvaLvaIleLysBsrOsrGlyAspAspArgTyr 40 ;  
; APPLICANT: C. Frank Bennett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS;  
Db 134 CAAGAGGGTTGAGAGTAGCTTGACTTAAACATCTGGATGATAC 193 ; FILE REFERENCE: RITS-0324  
; CURRENT APPLICATION NUMBER: US/09/966,451  
; CURRENT FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 88 ; SEQ ID NO 10  
; SEQ ID NO 11 LENGTH: 31000  
; SEQ ID NO 12 TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: US-09-966-451-10  
QY 41 AspGlnPheHisIleArgGlyAspGluIleLeuIleGlnThrGlyLysSerProThrSer 60 ;  
Db 194 ATTCAGTTTACATAGGAGTTGAGCTTCAACTGGAAAATCCACTCT 253 ;  
; LENGTH: 3133  
QY 61 GluLeuLeuPheAspTrpGlyThrThrAspGlyAspLeuValAspLeu 80 ;  
Db 254 GAATRACTGTTGACTGGGGACACAAATTGCACTGGATCTGGATCTTG 313 ;  
; LENGTH: 3133  
QY 81 IleGlnAspGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98 ;  
Db 314 ATCCAATGAAATTTGCTCCGAGCTTGTGCTCCAGATGCTGTCCC 367 ;  
; LENGTH: 3133  
**RESULT 2**  
US-09-966-451-3 ;  
; Sequence 3, Application US/09966451  
; Patent No. 6693959  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS;  
; FILE REFERENCE: RITS-0324  
; CURRENT APPLICATION NUMBER: US/09/966,451  
; CURRENT FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 88 ; SEQ ID NO 3  
; SEQ ID NO 4 LENGTH: 2817  
; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50) . . . (1432)  
; US-09-966-451-3  
Alignment Scores:  
Pred. No.: 2.68e-28 Length: 31000  
Score: 256.00 Matches: 49  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 98.00% Mismatches: 0  
Query Match: 49.52% Indels: 0  
DB: 4 Gaps: 0  
US-10-001-254-6 (1-98) x US-09-966-451-10 (1-31000)  
QY 45 IleArgGlyPheGluIleLeuIleGlnThrGlyYbsrProThrSerGluLeuPhe 64 ;  
Db 12263 TTAAGGGATTGAGCATCTCAACTGGAAAAGCCCTTCGAATCTTT 13022 ;  
; SEQ ID NO 5 AspTrpGlyThrThrAspCysThrValGlyAspLeuValAspLeuIleLeu 84  
; Db 13023 GACTGGGACACACATTCACAGTTGGTGTGATCTGIGATCTTATCCAAATGAA 13082 ;  
; SEQ ID NO 6  
QY 85 PhePheAlaProAlaSerIleLeuLeuPheCo 94 ;  
Db 13083 TTITTCCTCGAGTCCTTGTCCCC 13112 ;  
; LENGTH: 3133  
**RESULT 4**  
US-09-135-232-1 ;  
; Sequence 1, Application US/09135232  
; Patent No. 6262228  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Zhaodan  
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods  
; FILE REFERENCE: T98-019  
; CURRENT APPLICATION NUMBER: US/09/135,232  
; CURRENT FILING DATE: 1998-08-17  
; NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1 LENGTH: 2288  
; TYPE: DNA  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (64) . . . (1851)  
; US-09-135-232-1  
Alignment Scores:  
Pred. No.: 0.000102 Length: 2288  
Score: 96.50 Matches: 23  
Percent Similarity: 47.95% Conservative: 12  
Best Local Similarity: 31.51% Mismatches: 31  
Query Match: 18.67% Indels: 7  
DB: 3 Gaps: 1  
US-10-001-254-6 (1-98) x US-09-135-232-1 (1-2288)  
QY 8 ValGlyLeuIleArglyLeuSerAspPheIleAspProGlnGluGlyLysLeu 27 ;  
Db 135 CTCCGAGACCTCGGCTGCTGCTGAGCTTGTCCC 367 ;  
; LENGTH: 3133  
**RESULT 3**  
US-09-966-451-10 ;  
; LENGTH: 3133

QY 28 AlavalalaleLySlysProSerGlyAspAspArgTyranglPheHisIleArgArg 47  
 ; |||| :  
 ; GCAGAGAGACTTCAGC-----AGCTGGCTGGATGTTCCGCAT 234  
 ; 196  
 Db 48 PheglualaleLeuGlnThrGlyLysSerProThrSerGluLeuLeuPheAspTyrGly 67  
 ; |||| :  
 ; 235 ATTCGAACATPATGAGCAAGGTAAAGCTGAAAGAGAATTCTGCTGGCA 294  
 QY 68 ThrThrAsnCysThrValGlyAspIeuValAspLeuIeu 80  
 ; |||| :  
 Db 295 CAGAAACAGACCATCGGTGACCTTACAGGCTC 333

RESULT 5  
 US-09-863-549-1  
 Sequence 1, Application US/09863549  
 ; Patent No. 657644  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CAO, Zhaodan  
 ; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods  
 ; FILE REFERENCE: T98-019  
 ; CURRENT APPLICATION NUMBER: US/09/863,549  
 ; CURRENT FILING DATE: 2001-05-22  
 ; PRIOR APPLICATION NUMBER: 09/135,232  
 ; PRIOR FILING DATE: 1998-08-17  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2288  
 ; TYPE: DNA  
 ; ORGANISM: human  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (64)..(1851)  
 ; US-09-863-549-1

Alignment Scores:  
 Pred. No.: 0.000102 Length: 2288  
 Score: 96.50 Matches: 23  
 Percent Similarity: 47.95% Conservative: 12  
 Best Local Similarity: 31.53% Mismatches: 31  
 Query Match: 18.67% Indels: 7  
 DB: 4 Gaps: 1

US-10-001-254-6 (1-98) x US-09-863-549-1 (1-2288)

QY 8 ValGlyLeuIleLeuIeArgLysLeuSerAspPheIleAspProGlnGluGlyTyrIleAspLysIeu 27  
 ; ::||| :  
 ; 136 CTGGAGAGAGCTGGCTGTCCTGAGCGCCGCCCTGGCTGAGCCGCTG 195

Db 2B AlavalalaleLySlysProSerGlyAspAspArgTyranglPheHisIleArgArg 47  
 ; ::||| :  
 ; 196 GCAGAGAGACTTCAGC-----AGCTGGCTGGATGTTTCGTCAT 234

QY 48 PheglualaleLeuGlnThrGlyLysSerProThrSerGluLeuLeuPheAspTyrGly 67  
 ; |||| :  
 ; 235 ATTCGAACATPATGAGCAAGGTAAAGCTGAAAGAGAATTCTGCTGGCA 294

QY 68 ThrThrAsnCysThrValGlyAspIeuValAspLeuIeu 80  
 ; |||| :  
 Db 295 CAGAAACAGACCATCGGTGACCTTACAGGCTC 333

RESULT 6  
 US-08-980-060-1  
 ; Sequence 1, Application US/08980060  
 ; Patent No. 5965421  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: FENG, PING  
 ; APPLICANT: MUZIO, MARTA  
 ; APPLICANT: DIXIT, VISHVA M.  
 ; TITLE OF INVENTION: HUMAN IRAK-2  
 ; NUMBER OF SEQUENCES: 14

RESULT 7  
 US-09-07-105-1  
 ; Sequence 1, Application US/09307105  
 ; Patent No. 6222019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: FENG, PING  
 ; APPLICANT: MUZIO, MARTA  
 ; APPLICANT: DIXIT, VISHVA M.  
 ; TITLE OF INVENTION: HUMAN IRAK-2  
 ; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/980,060  
 FILING DATE: Herewith  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STERFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.101000/EKS/AJK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 1:  
 SSQUENCE CHARACTERISTICS:  
 LENGTH: 1806 base pairs  
 TYPE: nucleic acid  
 STRANDBNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 34..1803  
 ; US-08-980-060-1

Alignment Scores:  
 Pred. No.: 0.0423 Length: 1806  
 Score: 79.00 Matches: 22  
 Percent Similarity: 49.28% Conservative: 12  
 Best Local Similarity: 31.88% Mismatches: 19  
 Query Match: 15.28% Indels: 16  
 DB: 2 Gaps: 2

US-10-001-254-6 (1-98) x US-08-980-060-1 (1-1806)

QY 45 IleargArgPheglualaleLeuGlnThr--GlySerProThrSerGluLeuIeu 63  
 ; ::||| :  
 ; 157 CTGGAGAGACTTCAGTCCATGGACGGGTCAGGGCTGAGCATCACGGCGAGCTGCTG 216

Db 2B AlavalalaleLySlysProSerGlyAspAspArgTyranglPheHisIleArgArg 47  
 ; ::||| :  
 ; 217 TGCTGTGGCATCGGGAGCCACGGCCTGGACACTTGACCTCCCTGGCCCTG 276

QY 64 PheAspTyrGlyThrThrAsnCysThrValGlyAspIeuValAspLeuIeuLeuIeu 83  
 ; |||| :  
 ; 84 GluPhePheAlaProAlaSerLeuLeuLeu 93

Db 277 GAGCTCTACCGGGCTGGCATCACCTGAACTGGAAACGGCTCTGAAATCAGGT 336

QY 94 -----ProbAlaVal 97  
 ; |||| :  
 Db 337 CCCATCCAGCCTTCCTGACTCTG 363

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/307,185  
 FILING DATE: 02-Feb-2001  
 CLASSIFICATION: *<Unknown>*

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/980,060  
 FILING DATE: 02-Feb-2001  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.101000/EKS/AJK

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1806 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE: CDS  
 LOCATION: 34..1803

US-02-307-185-1

Alignment Scores:  
 Pred. No.: 0.0423  
 Score: 79.00  
 Percent Similarity: 49.28%  
 Best Local Similarity: 31.88%  
 Query Match: 15.28%  
 DB: 3  
 Gaps: 2

US-10-001-254-6 (1-98) x US-09-307-185-1 (1-1806)

QY 45 IleArgArgPheGluAlaLeuLeuGlnThr--GlyLySerProThrSerGluLeu 63  
 Db 157 CTGGCGAGATCAAGTCATGGCGAGCTGGCTGGACCTGGTGAGCTGGTGAGCTGTG 216

QY 64 PheAspPtpGlyLyrThrThrAspCysThValGlyAspLeuValAspLeuLeuLeu 83  
 Db 217 TGGTGGTGGGCCATGCCGCAACCCACGCTCAGCAACTGGGACCTCTGGCCCTG 276

QY 84 GluPhePheAlaProAlaLaserLeuLeuLeu 93  
 Db 277 GAGCTCTACGGGCTGCCAACATCATCTGAAGTGGAAACCGGCTCTGAATCAGGT 336

QY 94 ----- ProAlaLalaVal 97  
 Db 337 CCCATTCAGCCTTCCTGACTCTGTG 363

RESULT 8  
 US-09-773-753-1  
 Sequence 1, Application US/09773753  
 Patent No. 6653452

GENERAL INFORMATION:  
 APPLICANT: NI, JIAN  
 FENG, PING  
 MUZIO, MARTA  
 DIXIT, VISHVA M.  
 TITLE OF INVENTION: HUMAN IRAK-2

---

NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/773,753  
 FILING DATE: 02-Feb-2001  
 CLASSIFICATION: *<Unknown>*

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/980,060  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.101000/EKS/AJK

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1806 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE: CDS  
 LOCATION: 34..1803

US-09-773-753-1

Alignment Scores:  
 Pred. No.: 0.0423  
 Score: 79.00  
 Percent Similarity: 49.28%  
 Best Local Similarity: 31.88%  
 Query Match: 15.28%  
 DB: 4  
 Gaps: 2

US-10-001-254-6 (1-98) x US-09-773-753-1 (1-1806)

QY 45 IleArgArgPheGluAlaLeuLeuGlnThr--GlyLySerProThrSerGluLeu 63  
 Db 157 CTGGCGAGATCAAGTCATGGCGAGCTGGTGAGCTGGTGAGCTGTG 216

QY 64 PheAspPtpGlyLyrThrThrAspCysThValGlyAspLeuValAspLeuLeu 83  
 Db 217 TGGTGGTGGGCCATGCCGCAACCCACGCTCAGCAACTGGGACCTCTGGCCCTG 276

QY 84 GluPhePheAlaProAlaLaserLeuLeuLeu 93  
 Db 277 GAGCTCTACGGGCTGCCAACATCATCTGAAGTGGAAACCGGCTCTGAATCAGGT 336

QY 94 ----- ProAlaLalaVal 97  
 Db 337 CCCATTCAGCCTTCCTGACTCTGTG 363

RESULT 9  
 US-08-980-060-3  
 Sequence 3, Application US/08980060  
 Patent No. 596521  
 GENERAL INFORMATION:  
 APPLICANT: NI, JIAN  
 FENG, PING

APPLICANT: MUZIO, MARTA  
 APPLICANT: DIXIT, VISHVA M.  
 TITLE OF INVENTION: HUMAN IRAK-2  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P. L. L. C.  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/980,060  
 FILING DATE: Herewith  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3459 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLogy: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 34..1908  
 ;  
 ALIGNMENT SCORES:  
 PRED. NO.: 0.115  
 SCORE: 79.00  
 PERCENT SIMILARITY: 49.28%  
 BEST LOCAL SIMILARITY: 31.88%  
 QUERY MATCH: 15.28%  
 DB: 2  
 US-10-001-254-6 (1-98) x US-08-980-060-3 (1-3459)

QY 45 IleArgGargPheGluAlaLeuGlnThr--GlyLysSerProThrSerGluLeu 63  
 DB 157 CTGCGGAATCTAACGTCATGGCTGAGCCGCTGAGCATCACGGGAGCTGCG 216  
 QY 64 PheAspPrGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGln 83  
 DB 217 TGGTGTGGGCCATCGGCAGGCCACGGCTGCACTTGAACTCTCTGTGCCGCTG 276  
 QY 84 GluPhePheAlaProAlaSerLeuLeuLeu----- 93  
 DB 277 GAGCTCTACGGGCTGCCAGATCACCTGAACTGGAAACGGCTCTGAATCAGGT 336  
 QY 94 -----ProAspAlaVal 97  
 DB 337 CCCATTCCAGCCTRCCTGACTCTGTG 363  
 RESULT 10  
 US-09-307-185-3  
 Sequence 3 Application US/09307185  
 Patent No. 6222019  
 GENERAL INFORMATION:  
 APPLICANT: NI, JIAN  
 APPLICANT: FENG, PING  
 APPLICANT: MUZIO, MARTA  
 ;  
 RESULT 11  
 US-09-773-73-3  
 Sequence 3 Application US/09773753  
 Patent No. 6653452  
 GENERAL INFORMATION:  
 APPLICANT: NI, JIAN

FENG, PING ; Patent No. 5965421  
 MUZIO, MARTA ; GENERAL INFORMATION:  
 DIXIT, VISHVA M. ; APPLICANT: NI, JIAN  
 TITLE OF INVENTION: HUMAN IRAK-2 ; APPLICANT: FENG, PING  
 NUMBER OF SEQUENCES: 14 ; APPLICANT: MUZIO, MARTA  
 CORRESPONDENCE ADDRESS: ; APPLICANT: DIXIT, VISHVA M.  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. ; TITLE OF INVENTION: HUMAN IRAK-2  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600 ; NUMBER OF SEQUENCES: 14  
 CITY: WASHINGTON ; CORRESPONDENCE ADDRESS:  
 STATE: D.C. ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 COUNTRY: USA ; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 ZIP: 20005-3934 ; CITY: WASHINGTON  
 COMPUTER READABLE FORM: ; STATE: D.C.  
 MEDIUM TYPE: Floppy disk ; COUNTRY: USA  
 COMPUTER: IBM PC compatible ; ZIP: 20005-3934  
 OPERATING SYSTEM: PC-DOS/MS-DOS ; COMPUTER READABLE FORM:  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 ; MEDIUM TYPE: Floppy disk  
 CURRENT APPLICATION DATA: ; COMPUTER: IBM PC Compatible  
 APPLICATION NUMBER: US/09/773,753 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 FILING DATE: 02-Feb-2001 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CLASSIFICATION: <Unknown> ; CURRENT APPLICATION DATA:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/980,060 ; APPLICATION NUMBER: US/08/980,060  
 FILING DATE: <Unknown> ; FILING DATE: Herewith  
 ATTORNEY/AGENT INFORMATION: ; CLASSIFICATION: 435  
 NAME: STEFFE, ERIC K. ; ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 36,688 ; NAME: STEFFE, ERIC K.  
 REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK ; REGISTRATION NUMBER: 36,688  
 TELECOMMUNICATION INFORMATION: ; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK  
 TELEPHONE: (202) 371-2600 ; TELECOMMUNICATION INFORMATION:  
 TELEFAX: (202) 371-2540 ; TELEPHONE: (202) 371-2600  
 INFORMATION FOR SEQ ID NO: 3: ; TELEFAX: (202) 371-2540  
 SEQUENCE CHARACTERISTICS: ; INFORMATION FOR SEQ ID NO: 14:  
 LENGTH: 3459 base pairs ; SEQUENCE CHARACTERISTICS:  
 TYPE: nucleic acid ; LENGTH: 479 base pairs  
 STRANDEDNESS: double ; TYPE: nucleic acid  
 TOPOLOGY: linear ; STRANDEDNESS: double  
 MOLECULE TYPE: DNA (genomic) ; TOPOLOGY: linear  
 FEATURE: ; MOLECULE TYPE: cDNA  
 NAME/KEY: CDS ; FEATURE:  
 LOCATION: 34..1908 ; NAME/KEY:  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-773-753-3 ; LOCATION:  
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 Pred. No.: 0.115 ; Length: 3459  
 Score: 79.00 ; Matches: 22  
 Percent Similarity: 49.28% ; Conservative: 12  
 Best Local Similarity: 31.88% ; Mismatches: 19  
 Query Match: 15.28% ; Insertions: 16  
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 US-10-001-254-6 (1-98) x US-09-773-753-3 (1-3459)  
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 Db 157 CTGGCGGAGATCAGTCATCTGAGCCGGTGAGGGTGAGCATACGGGGAGCTGCTG 216  
 QY 64 PheAspTrpGlyThrThrAsnCysThrVal3IlyAspLeuValAspLeuLeuGlnAsn 83  
 Db 217 TGGTGTGGGCACTGGGGCAGCCACGTCAGCAACTTGAGGACTCTCTGGCCCTG 276  
 QY 84 GluPhePheAlaProAlaSerLeuLeu 93  
 Db 277 GAGCTCTACCGGGCTGCCAGTCATCTGAACTGGAAACGGCTCTGAATCAGGT 336  
 QY 94 -----IroASpAlaVal 97  
 Db 337 CCCATTCAGCTCCCTGACAGCTG 363  
 RESULT 12 ; Sequence 14, Application US/08980060  
 US 08-980-060-14/c ; Patent No. 6222019  
 ; Sequence 14, Application US/09307185  
 ; General Information:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: FENG, PING  
 ; APPLICANT: MUZIO, MARTA  
 ; APPLICANT: DIXIT, VISHVA M.  
 ; TITLE OF INVENTION: HUMAN IRAK-2  
 ; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STEINE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/307,185  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/980,060  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540

SEQUENCE CHARACTERISTICS:  
 LENGTH: 479 base pairs  
 TOPOLogy: linear  
 STRANDEDNESS: double  
 MOLECULE TYPE: nucleic acid  
 STRANDEDNESS: double  
 MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-09-307-185-14

Alignment Scores:  
 Pred. No.: 0.00664 Length: 479  
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 DB: 3 Gaps: 1

US-10-001-254-6 (1-98) x US-09-307-185-14 (1-479)

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Qy 64 PheAspPrglyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsn 83  
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Qy 84 GluPhePheAlaProAlaSerIleLeuLeu 93  
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RESULT 14  
 US-09-773-753-14/c  
 GENERAL INFORMATION:  
 Sequence 14: Application US/09773-753  
 ; Patent No. 6653152  
 ; Sequence 14, Application US/09773-753  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; FENG, PING  
 ; MUZIO, MARTA  
 ; DIXIT, VISHVA M.  
 ; TITLE OF INVENTION: HUMAN IRAK-2  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STEINE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: D.C.

COUNTRY: USA  
 ZIP: 20005-3334

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/773,753  
 FILING DATE: 02-Feb-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/980,060  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540

SEQUENCE CHARACTERISTICS:  
 LENGTH: 479 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLogy: linear  
 STRANDEDNESS: double  
 MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-09-773-753-14

Alignment Scores:  
 Pred. No.: 0.00664 Length: 479  
 Score: 78.50 Matches: 19  
 Percent Similarity: 60.00% Conservative: 11  
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 Query Match: 15.18% Indels: 1  
 DB: 4 Gaps: 1

US-10-001-254-6 (1-98) x US-09-773-753-14 (1-479)

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Qy 64 PheAspPrglyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsn 83  
 Db 184 TGGTGGTGGGGCATGGGGAGCCACCGGCCAGCTGCACACTTGTCACCTCTGCGCGCTG 125

Qy 84 GluPhePheAlaProAlaSerIleLeuLeu 93  
 Db 124 GAGCTCTACGGGGCTGCCAGATCATCTG 95

RESULT 15  
 US-09-214-808-1  
 Sequence 1, Application US/09214808A  
 ; Patent No. 6475793  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roenthal, Andre  
 ; APPLICANT: Freiberg, Christoph  
 ; APPLICANT: Perret, Xavier Philippe  
 ; APPLICANT: Broughton, William John  
 ; TITLE OF INVENTION: Genomic Sequence of Rhizobium sp. NGR 234 Symbiotic  
 ; Patent No. 6475793  
 ; TITLE OF INVENTION: Plasmid  
 ; FILE REFERENCE: CARP0058  
 ; CURRENT APPLICATION NUMBER: US/09/214,808A  
 ; CURRENT FILING DATE: 1999-06-22  
 ; PRIOR APPLICATION NUMBER: PCT/IB97/00950  
 ; PRIOR FILING DATE: 1997-07-10  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 1

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; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
; US-09-214-808-1
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## Alignment Scores:

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Percent Similarity:	47.06%	Conservative:	12
Best Local Similarity:	32.94%	Mismatches:	39
Query Match:	13.93%	Indices:	6
DB:	4	Gaps:	5

US-10-001-254-6 (1-98) x US-09-214-808-1 (1-536165)

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Db      97239 ATAGAGCATGGGAGACTTGGAAGGAGAAATCAGTGTGCTCAAGCTCCCTGAC 97298
QY      36 --GLYAspDspArg--TyrAsnGlnPheHisIleArgLysPheGluIalaLeuGln 53
Db      97299 ACCGGCGGAGTCACATGACTTGACTTGCCCTGAGATCCACAGATAATCACCTGTTAG 97358
QY      54 ThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThrVal 73
Db      97359 ATTAGGCCCTGGCTCAACTTAGATGCTCTTGATGG--TCTACTACTGCGCTCAA 97415
QY      74 --GLYAspIleuValAspIleuLeuIleGlnAspGluPheAlaProIleAspLeuIleu 92
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Search completed: January 12, 2005, 08:54:30  
 Job time : 157 secs



ORIGIN

Alignment Scores:	1.4e-61	Length:	294
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Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:			

US-10-001-254-6 (1-98) x ARX431296 (1-294)

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LOCUS	DEFINITION	SEQUENCE	15 from Patent	W0240580.		
Db	ACATATGCGCGCTCAATGTRGACTTAATTGAGCTTATGCT	60				
QY	21 GlngluglyTrpLysLeuAlaValAlaLysProSerGlyAspAspArgTyr	40				
QY	61 CAGAGAGATGGAGAAGTAGCTGTAGCTTAAACCATCTGATGATA	133				
QY	41 AenGlnpheHisIleLeuGluPheAlaProLaserLeuLeuProAlaValPro	98				
QY	61 CAGAGAGATGGAGAAGTAGCTGTAGCTTAAACCATCTGATGATA	313				
Db	ATCCAAATGATTTTCTCTCAGTCAGTCTTGCTCCAGATGCTTCCC	367				

RESULT 2

AR223870	AR223870	AR223870	833 bp	DNA	linear	PAT 26-SBP-2002
DEFINITION	Sequence 10 from patent US 640663.	SEQUENCE				
VERSION	AR223870.1	AR223870.1	GI:23332452			
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1. (bases 1 to 833)					
AUTHORS	Scanlan,M.J., Stockert,E., Chen,Y.-T., Old,L.J., Jager,B. and Knuth,A.					
TITLE	Renal cancer associated antigens and uses therefor					
JOURNAL	Patent: US 640663-A 10 27-aug-2002;					
FEATURES	Location/Qualifiers					
source	1. .833 /organism="unknown" /mol_type="genomic DNA"					

ORIGIN

Alignment Scores:	4.94e-61	Length:	833
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Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:			

US-10-001-254-6 (1-98) x AR223870 (1-833)

RESULT 3	AX431306	AX431306	1383 bp	DNA	linear	PAT 28-JUN-2002
LOCUS	DEFINITION	SEQUENCE	15 from Patent	W0240580.		
Db	ACATATGCGCGCTCAATGTRGACTTAATTGAGCTTATGCT	60				
QY	81 IlegInasnglPheAlaProLaserLeuLeuProAlaValPro	98				
QY	61 CAGAGAGATGGAGAAGTAGCTGTAGCTTAAACCATCTGATGATA	313				
Db	ATCCAAATGATTTTCTCTCAGTCAGTCTTGCTCCAGATGCTTCCC	367				

ORIGIN

Alignment Scores:	9.14e-61	Length:	1383
Pred. No.:	517.00	Matches:	98
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:			

US-10-001-254-6 (1-98) x ARX431306 (1-1383)

RESULT 3	AX431306	AX431306	1383 bp	DNA	linear	PAT 28-JUN-2002
LOCUS	DEFINITION	SEQUENCE	15 from Patent	W0240580.		
Db	ACATATGCGCGCTCAATGTRGACTTAATTGAGCTTATGCT	60				
QY	1 ThnTYrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheLeaPro	20				
QY	74 ACATATGCGCGCTCAATGTRGACTTAATTGAGCTTATGCT	133				
QY	21 GlngluglyTrpLysLeuAlaValAlaLysProSerGlyAspAspArgTyr	40				
QY	85 CAGAGAGATGGAGAAGTAGCTGTAGCTTAAACCATCTGATGATA	144				
Db	41 AenGlnpheHisIleLeuGluPheAlaProLaserLeuLeuProAlaValPro	98				
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ORIGIN

Alignment Scores:	1.4e-61	Length:	294
Pred. No.:	517.00	Matches:	98
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:			

US-10-001-254-6 (1-98) x ARX431306 (1-294)

RESULT 3	AX431306	AX431306	1383 bp	DNA	linear	PAT 28-JUN-2002
LOCUS	DEFINITION	SEQUENCE	15 from Patent	W0240580.		
Db	ACATATGCGCGCTCAATGTRGACTTAATTGAGCTTATGCT	60				
QY	81 IlegInasnglPheAlaProLaserLeuLeuProAlaValPro	98				
QY	61 CAGAGAGATGGAGAAGTAGCTGTAGCTTAAACCATCTGATGATA	313				
Db	ATCCAAATGATTTTCTCTCAGTCAGTCTTGCTCCAGATGCTTCCC	367				

Db	RESULT 4	BC013316	205	GAATTCTTGTGACTGGGCACCAAAATGAGCTGGTACCTGGATCTTC	264
Qy	LOCUS	BC013316	6	/lab_host="DH10B"	
DEFINITION	Homo sapiens interleukin-1 receptor-associated kinase 4 (mRNA)			/note="Vector: pDNR-LIB"	
ACCESION	clone MGC:13330 IMGR:4287014, complete cds.			1. 1629	
VERSION	BC013316.1 GI:15426431			/gene="IRAK4"	
KEYWORDS	MGC.			/note="Synonyms: NY-REN-64, REN64"	
SOURCE	Homo sapiens (human)			/db_xref="locusID:51135"	
ORGANISM	Homo sapiens			/ab_xref="NM:606883"	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1629)			71..1453	
AUTHORS	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Sheppard C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordon H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina A., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casevant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loqueland N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEvans P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lin X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalicka U., Smilus D.E., Schnurch A., Schein J.E., Jones S.J. and Marra M.A.			/db_xref="MM:606883"	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			/translation="MKKPTSTVYRCLNVGLIRKLSDFIPQEGKMKLAVAKRPSGDTRFNSFSFLKNTNFEDPNSVGGNGESEFGVWVKGYANTTAVKLAAMDDRYNQPHIRSLPEALQTQVOKPDRMTMPTVONLSOSYMPDSPPSSPASLVEYDVTTBKQPDQBEKMKCQHNEVLLPGPSGDDCLIVYVNPMSLUDLRSCLDGTPPLSWHRCKTQDQGAANGIHFENHLHIDRKSANTSALVFTPKSDFGVLVLIITGLPAVDEBRASEBKAQTVMSRSVIGSTTMAPELGETTPKSDTISFGVLUVLIITGLPAVDEBPOLLQDKEBEDKEVNIEDYTDIKNDADSTSVEAMYSVASOQJHEKONKRDPICKVQQLQEMTAS"	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			ORIGIN	
PUBLISHED	2 (bases 1 to 1629)			Alignment Scores:	
REFERENCE	Stratberg R.			Pred. No.: 1.11e-60	Length: 1629
AUTHORS	Direct Submission.			Score: 517.00	Matches: 98
COMMENT	Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			Percent Similarity: 100.00%	Conservative: 0
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			Best Local Similarity: 100.00%	Mismatches: 0
TITLE	Contact: MGC help desk			Query Match: 100.00%	Indels: 0
JOURNAL	Email: cgpb@MAIL.nih.gov			DB:	Gaps: 0
PUBLISHED	Tissue Procurement: ARCC		US-10-001-254-6 (1-98) x BC013316 (1-1629)		
REFERENCE	cDNA Library Preparation: CLONTECH Laboratories, Inc.	Qy	1	Alignment Scores:	
AUTHORS	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMU)	Db	41	Pred. No.: 1.11e-60	Length: 1629
COMMENT	DNA Sequencing by: Institute for Systems Biology	Db	95	Score: 517.00	Matches: 98
REMARK	http://www.systemsbiology.org	Db	215	Percent Similarity: 100.00%	Conservative: 0
TITLE	contact: amada@systemsbiology.org	Db	21	Best Local Similarity: 100.00%	Mismatches: 0
JOURNAL	Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting	Db	155	Query Match: 100.00%	Indels: 0
PUBLISHED	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIMU at: http://image.limn.gov	Db	41	Query Match: 100.00%	Gaps: 0
REFERENCE	Series: ITAL Plate: 19 Row: n Column: 24	Db	41	Alignment Scores:	
AUTHORS	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705840.	Db	275	Pred. No.: 1.11e-60	Length: 1629
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AUTHORS	Chuang, T.H. and Ulevitch, R.J.	Db	334	Best Local Similarity: 100.00%	Mismatches: 0
TITLE	Human interleukin-1 receptor associated kinase 4 cDNA sequences	Db	334	Query Match: 100.00%	Indels: 0
JOURNAL	Unpublished	Db	334	DB:	Gaps: 0
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AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	Db	334	Percent Similarity: 100.00%	Conservative: 0
TITLE	Human interleukin-1 receptor associated kinase 4 cDNA sequences	Db	334	Best Local Similarity: 100.00%	Mismatches: 0
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REFERENCE	2 (bases 1 to 1636)	Db	334	DB:	Gaps: 0



ACCESSION C0728380  
 VERSION C0728380.1 GI:42297030  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcheria; Primates; Cetartochini; Hominidae; Homo.  
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
 TITLE KITS, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  
 JOURNAL Patent: WO 02068579-A 14314 06-SEP-2002;  
 PE Corporation (NY) (US)  
 FEATURES Location/Qualifiers  
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 Query Match: 100.00% Indels: 0  
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 Db 254 GATTTACCTTTGACTGGGCCACCAATTCGAGCTGGATCTTGATGCTTGTG 313  
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 RESULT 9  
 AX431318  
 LOCUS AX431318  
 DEFINITION Sequence 27 from Patent WO0240680. DNA linear PAT 28-JUN-2002  
 ACCESSION AX431318  
 VERSION AX431318.1 GI:2165187  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcheria; Primates; Cetartochini; Hominidae; Homo.  
 TITLE Novel death domain Proteins  
 JOURNAL Roth, W. and Steiner-Liewen, F.  
 Db 216 GAATCTGTTGACTGGGCCACCAATTCGAGCTGGATCTTGATGCTTGTG 275  
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 LOCUS AR475548  
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 VERSION AR475548  
 AUTHORS AR475548.1 GI:42715031  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 2817)  
 AUTHORS Bennett, C.F. and Preier, S.M.  
 TITLE Antisense modulation of IL-1 receptor-associated kinase-4 expression  
 JOURNAL Patent: US 6692959-A 3 17-FEB-2004;  
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 Score: 517.00 Matches: 98  
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 DB: Gaps: 0

DB:	6	Gaps:	0
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QY	74 Aspartic acid-rich domain	20	Pred. No.: 2.17e-60
QY	74 ACATATGCGCTGCCTCAAGTTGGACTAAATTAGGAGCTTCAGATTGATCCT	133	Score: 517.00
QY	21 Glu-Glu-Gly-Tyr-Lys-Lys-Lys-Lys-Lys-Pro-Ser-Gly-Yas-Pasp-Ag-Tyr	40	Percent Similarity: 100.00%
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QY	41 Aspar-Asp-His-Ile-Gly-Arg-Phe-Glu-alu-leu-Gln-thr-Gly-Lys-Ser-Pro-Thr-Ser	60	Query Match: 100.00%
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Db	314 ATCCAAATGAA-TTGTGCTCCTCGAGCTTGTCTCCAGATCTGTTCCC	367	Indels: 0
RESULT 10			
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DEFINITION	Homo sapiens putative protein kinase NY-REN-64 antigen mRNA,	linear	PrI 05-JAN-2000
ACCESSION	complete cds.		
VERSION	AP155118		
KEYWORDS	AF155118.1 GI:53360130		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2817)		RESULT 11
AUTHORS	Scanlan, M.J., Gordian, J.D., Williamson, B., Stockert, E., Bander, N.H., Jongeneel, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T., and Old, L.J.		AK000528
TITLE	Antigens recognized by autologous antibody in patients with renal-cell carcinoma		DEFINITION
JOURNAL	Int. J. Cancer 83 (4), 456-464 (1999)		Homo sapiens cDNA FLJ20521, fis, clone KAT10395.
MEDLINE	99438124		ACCESSION
PUBMED	10504779		AK000528
REFERENCE	2 (bases 1 to 2817)		VERSION
AUTHORS	Scanlan, M.J., Gordian, J.D., Williamson, B., Stockert, E., Bander, N.H., Jongeneel, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T., and Old, L.J.		AK000528.1 GI:7020683
TITLE	Direct submission		KEYWORDS
JOURNAL	Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA		Homo sapiens (human)
FEATURES	Location/Qualifiers		SOURCE
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/codon_start=1			Unpublished
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QY 21 GlngIuglyTrpLysLysLeuAlaValAlaLysLysProSerGlyAspPaspTyr 40		
Db 85 CAAGAAGGATGCGAGAGTAGCTGAGCTTAATTAAACCATCTGGTGAATGATAC 144		
QY 41 AsngInpheHisIleArgPheGluAlaLeuLeuGlnThrGlyLysSerProSer 60		
Db 145 ATCACATTCACTAGGAGTTGAGCATRACTCAACTTGGAAGAACGCCACTCT 204		
QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80		
Db 205 GAATTACTGTTGACTGGGACCACTGACATCTGGATCTGTGATCTTG 264		
ORIGIN		
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DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 (IRAK4), mRNA, complete cds.		
ACCESSION AF445802		
VERSION AF445802.1	GT:20219009	
KEYWORDS		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE 1 (bases 1 to 1383)	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homidae; Homo.	
AUTHORS Li, S., Streilow, A., Fontana, E.J. and Wasche, H.	IRAK-4: a novel member of the IRAK family with the properties of an IRAK-kinase	
TITLE Proc. Natl. Acad. Sci. U.S.A. 99 (8), 5567-5572 (2002)		
JOURNAL MEDLINE	21957277	
LOCUS AY283670	1383 bp mRNA linear PRI 17-JUN-2003	
PUBLISHED 1196013	1196013 (bases 1 to 1383)	
REFERENCE 2	(bases 1 to 1383)	
AUTHORS Mirsuki,N., Suruki,S., Duncan,G.S., Millar,D.G., Wada,T.,	Mak,T.W. and Yeh,W.C.	
	Wesche,H., Ohashi,P.S., Itie,A., Li,S., Penninger,J.M.,	
	Severe impairment of interleukin-1 and Toll-like receptor	
	Signalling in mice lacking IRAK-4	
TITLE JOURNAL Nature 416 (6882), 750-756 (2002)	21959395	
PUBLISHED 11923871	11923871 (bases 1 to 1383)	
REFERENCE 3	Li,S., Streilow,A., Fontana,E.J. and Wesche,H.	
AUTHORS Direct Submission	Submitted (08-NOV-2001) BIOLOGY I, Tularik Inc., 2 Corporate Drive,	
JOURNAL South San Francisco, CA 94080, USA	Location/Qualifiers	
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ORIGIN		
	QY 1 ThrtYvalArgCysLeuLeuValGlyLeuLeuArgLysLeuSerAspPheIleAspPro 20	
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	QY 21 GlngIuglyTrpLysLysLeuAlaValAlaLysLysProSerGlyAspPaspTyr 40	
	Db 85 CAAGAAGGATGCGAGAGTAGCTGAGCTTAATTAAACCATCTGGTGAATGATAC 144	
	QY 41 AsngInpheHisIleArgPheGluAlaLeuLeuGlnThrGlyLysSerProSer 60	
	Db 145 ATCACATTCACTAGGAGTTGAGCATRACTCAACTTGGAAGAACGCCACTCT 204	
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DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 mutant form 1 (IRAK4) mRNA, complete cds.

ACCESSION AY283670  
VERSION AY283670.1 GI:31871817

KEYWORDS KEYWORD SOURCE  
ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Cattarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1383)  
AUTHORS Medvedev,A.B., Lentschait,A., Kuhns,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Ardit,M., Gallin,J.I. and Vogel,S.N.

TITLE Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections

JOURNAL J. Exp. Med. (2003) In press

REFERENCE 2 (bases 1 to 1383)  
AUTHORS Medvedev,A.B., Lentschait,A., Kuhns,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Ardit,M., Gallin,J.I. and Vogel,S.N.

JOURNAL Direct Submission  
Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA

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ORIGIN ORIGIN

Alignment Scores:  
Pred. No.: 3.24e-60 Length: 1383  
Score: 513.00 Matches: 97  
Percent Similarity: 98.98% Conservative: 0  
Best Local Similarity: 98.98% Mismatches: 1  
Query Match: 9.23% Indels: 0  
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AY283670 (1-1383)

Db 85 CAAGAGATGGAGAACGTTAGCTTAAACCACTGGATGATGATAC 144  
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